

EG327	MNKIYRIIWN	SALNAWVAVS	ELTRNHTKRA	SATVATAVLA	TLLFATVQAS	50
BZ198	MNKIYRIIWN	SALNAWVVVS	ELTRNHTKRA	SATVATAVLA	TLLFATVQAN	
BZ10	MNKISRIIWN	SALNAWVVVS	ELTRNHTKRA	SATVATAVLA	TLLFATVQAN	
H15	MNKIYRIIWN	SALNAWVVVS	ELTRNHTKRA	SATVATAVLA	TLLFATVQAN	
EG329	MNEILRIIWN	SALNAWVVVS	ELTRNHTKRA	SATVATAVLA	TLLFATVQAN	
PMC21	MNKIYRIIWN	SALNAWVVVS	ELTRNHTKRA	SATVKTAVLA	TLLFATVQAS	
H38	MNKIYRIIWN	SALNAWVAVS	ELTRNHTKRA	SATVKTAVLA	TLLFATVQAN	
P20	MNKIYRIIWN	SALNAWVVVS	ELTRNHTKRA	SATVATAVLA	TLLSATVQAN	
Z2491	MNKIYRIIWN	SALNAWVAVS	ELTRNHTKRA	SATVKTAVLA	TLLFATVQAN	
H41	MNKIYRIIWN	SALNAWVAVS	ELTRNHTKRA	SATVKTAVLA	TLLFATVQAN	
Consensus	<u>MN-I-RIIWN</u>	<u>SALNAWV-VS</u>	<u>ELTRNHTKRA</u>	<u>SATV-TAVLA</u>	<u>TLL-ATVQA-</u>	

C1

	51		100
EG327	TTDDD...DL	YLEPVQRTAV	VLSFRSDKEG TGEKE.VTED SNWGVYFDKK
BZ198	ATDDD...DL	YLEPVQRTAV	VLSFRSDKEG TGEKE.GTED SNWAVYFDEK
BZ10	ATDDD...DL	YLEPVQRTAV	VLSFRSDKEG TGEKE.GTED SNWAVYFDEK
H15	ATDDD...DL	YLEPVQRTAV	VLSFRSDKEG TGEKE.GTED SNWAVYFDEK
EG329	ANNEEQEEDL	YLDPVLRIVA	VLIVNSDKEG TGEKEKVEEN SDWAVYFNEK
PMC21	ANNEEQEEDL	YLDPVQRTVA	VLIVNSDKEG TGEKEKVEEN SDWAVYFNEK
H38	ATDED...EEE	ELEPVRSAL	VLQFMIDKEG NGENE.STGN IGWSIYYDHN
P20	ATDTD...EDE	ELESVARSA	VLQFMIDKEG NGEIESTGDI GWSIYYDDHN
Z2491	ATDED...EEE	ELESVQR.SV	VGSIQASMEG SGELET...I SLSMTNDSKE
H41	ATDED...EEE	ELESVQR.SV	VGSIQASMEG SVELET...I SLSMTNDSKE
Consensus	-----	<u>-L--V-R--</u>	<u>V-----EG --E-E-----</u>

V1

	101		150
EG327	GVLTAGITL	KAGDNLKIKQ	NTNENTNASS ....FTYSLK KDLTDLTSVG
BZ198	RVLKAGAITL	KAGDNLKIKQ	NTNENTNDSS ....FTYSLK KDLTDLTSVE
BZ10	RVLKAGAITL	KAGDNLKIKQ	NTNENTNENT NDSSFTYSLK KDLTDLTSVE
H15	RVLKAGAITL	KAGDNLKIKQ	NTNENTNENT NDSSFTYSLK KDLTDLTSVE
EG329	GVLTAAREITL	KAGDNLKIKQ	NG...TN... ....FTYSLK KDLTDLTSVG
PMC21	GVLTAAREITL	KAGDNLKIKQ	NG...TN... ....FTYSLK KDLTDLTSVG
H38	NTLHGATVTL	KAGDNLKIKQ	NTNKNNTNENT NDSSFTYSLK KDLTDLTSVE
P20	TLHG.ATVTL	KAGDNLKIKQ	SGKD..... ....FTYSLK KELKDLTSVE
Z2491	FVDPYIVVTL	KAGDNLKIKQ	NTNENTNASS ....FTYSLK KDLTGLINVE
H41	FVDPYIVVTL	KAGDNLKIKQ	NTNENTNASS ....FTYSLK KDLTGLINVE
Consensus	-----	<u>TL KAGDNLKIKQ</u>	----- <u>FTYSLK K-L--L--V-</u>
	V1	C2	V2 C3

	151		200
EG327	TEKLSFSANS	NKVNITSDTK	GLNFAKKTAE TNGDPTVHLN GIGSTLTDTL
BZ198	TEKLSFGANG	NKVNITSDTK	GLNFAKETAG TNGDPTVHLN GIGSTLTDTL
BZ10	TEKLSFGANG	NKVNITSDTK	GLNFAKETAG TNGDPTVHLN GIGSTLTDTL
H15	TEKLSFGANG	NKVNITSDTK	GLNFAKETAG TNGDPTVHLN GIGSTLTDTL
EG329	TEKLSFSANG	NKVNITSDTK	GLNFAKETAG TNGDPTVHLN GIGSTLTDTL
PMC21	TEKLSFSANG	NKVNITSDTK	GLNFAKETAG TNGDPTVHLN GIGSTLTDTL
H38	TEKLSFGANG	NKVNITSDTK	GLNFAKETAG TNGDPTVHLN GIGSTLTDTL
P20	TEKLSFGANG	NKVNITSDTK	GLNFAKETAG TNGDPTVHLN GIGSTLTDTL
Z2491	TEKLSFGANG	KKVNIIISDTK	GLNFAKETAG TNGDPTVHLN GIGSTLTDML
H41	TEKLSFGANG	KKVNIIISDTK	GLNFAKETAG TNGDPTVHLN GIGSTLTDML
Consensus	<u>TEKLSF-AN-</u>	<u>-KVNII-SDTK</u>	<u>GLNFAK-TA- TNGD-TVHLN GIGSTLTD-L</u>

C3

FIG. 1

201 250

EG327	LNTGATTNVT	NDNVTDDDEKK	RAASVKDVLN	AGWNIKGVKP	GTTAS..DNV
BZ198	LNTGATTNVT	NDNVTDDDEKK	RAASVKDVLN	AGWNIKGVKP	GTTAS..DNV
BZ10	LNTGATTNVT	NDNVTDDDEKK	RAASVKDVLN	AGWNIKGVKP	GTTAS..DNV
H15	LNTGATTNVT	NDNVTDDDEKK	RAASVKDVLN	AGWNIKGVKP	GTTAS..DNV
EG329	LNTGATTNVT	NDNVTDDDEKK	RAASVKDVLN	AGWNIKGVKP	GTTAS..DNV
PMC21	LNTGATTNVT	NDNVTDDDEKK	RAASVKDVLN	AGWNIKGVKP	GTTAS..DNV
H38	LNTGATTNVT	NDNVTDDDEKK	RAASVKDVLN	AGWNIKGVKP	GTTAS..DNV
P20	AGSSASHVDA	GNQST..HYT	RAASIKDVLN	AGWNIKGVKP	GTTAS..DNV
Z2491	AGSSASHVDA	GNQST..HYT	RAASIKDVLN	AGWNIKGVKP	GTTAS..DNV
H41	LNTGATTNVT	NDNVTDDDEKK	RAASVKDVLN	AGWNIKGVKP	GTTAS..DNV
Consensus	----A-----	----T-----	RAAS-KDVLN	AGWNIKGVK-	G-T-----NV

V3 C4 V4

251 300

EG327	DFVRTYDTVE	FLSADTKTTT	VNVEKDNKG	RTEVKIGAKT	SVIKEKDGKL
BZ198	DFVRTYDTVE	FLSADTKTTT	VNVEKDNKG	RTEVKIGAKT	SVIKEKDGKL
BZ10	DFVRTYDTVE	FLSADTKTTT	VNVEKDNKG	RTEVKIGAKT	SVIKEKDGKL
H15	DFVRTYDTVE	FLSADTKTTT	VNVEKDNKG	RTEVKIGAKT	SVIKEKDGKL
EG329	DFVRTYDTVE	FLSADTKTTT	VNVEKDNKG	RTEVKIGAKT	SVIKEKDGKL
PMC21	DFVRTYDTVE	FLSADTKTTT	VNVEKDNKG	RTEVKIGAKT	SVIKEKDGKL
H38	DFVRTYDTVE	FLSADTKTTT	VNVEKDNKG	RTEVKIGAKT	SVIKEKDGKL
P20	DFVRTYDTVE	FLSADTKTTT	VNVEKDNKG	RTEVKIGAKT	SVIKEKDGKL
Z2491	DFVRTYDTVE	FLSADTKTTT	VNVEKDNKG	RTEVKIGAKT	SVIKEKDGKL
H41	DFVRTYDTVE	FLSADTKTTT	VNVEKDNKG	RTEVKIGAKT	SVIKEKDGKL
Consensus	DFV-TYDTVE	FLSADTKTTT	VNVEKDNKG	-TEVKIGAKT	SVIKEKDGKL

C5

301 350

EG327	VTGKDKGENG	SSTDKEGGLV	TAKEVIDAVN	KAGWRMKTTT	ANGQTGOADK
BZ198	VTGKDKGENG	SSTDKEGGLV	TAKEVIDAVN	KAGWRMKTTT	ANGQTGOADK
BZ10	VTGKDKGENG	SSTDKEGGLV	TAKEVIDAVN	KAGWRMKTTT	ANGQTGOADK
H15	VTGKDKGENG	SSTDKEGGLV	TAKEVIDAVN	KAGWRMKTTT	ANGQTGOADK
EG329	VTGKDKGENG	SSTDKEGGLV	TAKEVIDAVN	KAGWRMKTTT	ANGQTGOADK
PMC21	VTGKDKGENG	SSTDKEGGLV	TAKEVIDAVN	KAGWRMKTTT	ANGQTGOADK
H38	VTGKDKGENG	SSTDKEGGLV	TAKEVIDAVN	KAGWRMKTTT	ANGQTGOADK
P20	VTGKDKGENG	SSTDKEGGLV	TAKEVIDAVN	KAGWRMKTTT	ANGQTGOADK
Z2491	VTGKDKGENG	SSTDKEGGLV	TAKEVIDAVN	KAGWRMKTTT	ANGQTGOADK
H41	VTGKDKGENG	SSTDKEGGLV	TAKEVIDAVN	KAGWRMKTTT	ANGQTGOADK
Consensus	VTGK-K-EN-	SSTD-GEGLV	TAKEVIDAVN	KAGWRMKTTT	ANGQTGOADK

C5

351 400

EG327	FETVTSGTNV	TFASGKGTTA	TVSKDDQGN	TVMYDVNVGD	ALNVNQLQNS
BZ198	FETVTSGTNV	TFASGKGTTA	TVSKDDQGN	TVKYDVNVGD	ALNVNQLQNS
BZ10	FETVTSGTKV	TFASGNGTTA	TVSKDDQGN	TVKYDVNVGD	ALNVNQLQNS
H15	FETVTSGTKV	TFASGNGTTA	TVSKDDQGN	TVKYDVNVGD	ALNVNQLQNS
EG329	FETVTSGTNV	TFASGKGTTA	TVSKDDQGN	TVMYDVNVGD	ALNVNQLQNS
PMC21	FETVTSGTNV	TFASGKGTTA	TVSKDDQGN	TVMYDVNVGD	ALNVNQLQNS
H38	FETVTSGTNV	TFASGKGTTA	TVSKDDQGN	TVKYDVNVGD	ALNVNQLQNS
P20	FETVTSGTKV	TFASGNGTTA	TVSKDDQGN	TVKYDVNVGD	ALNVNQLQNS
Z2491	FETVTSGTNV	TFASGKGTTA	TVSKDDQGN	TVMYDVNVGD	ALNVNQLQNS
H41	FETVTSGTKV	TFASGNGTTA	TVSKDDQGN	TVKYDVNVGD	ALNVNQLQNS
Consensus	FETVTSGT-V	TFASG-GTTA	TVSKDDQGN	TV-YDVNVGD	ALNVNQLQNS

C5

**FIG. 1 cont.**

EG327	GNLDSKAVA	GSSGKVISGN	VSPSKGKMDE	TVNINAGNNI	EITRNGKNID	450
BZ198	GWNLDSKAVA	GSSGKVISGN	VSPSKGKMDE	TVNINAGNNI	EITRNGKNID	
BZ10	GWNLDSKAVA	GSSGKVISGN	VSPSKGKMDE	TVNINAGNNI	EITRNGKNID	
H15	GWNLDSKAVA	GSSGKVISGN	VSPSKGKMDE	TVNINAGNNI	EITRNGKNID	
EG329	GWNLDSKAVA	GSSGKVISGN	VSPSKGKMDE	TVNINAGNNI	EITRNGKNID	
PMC21	GWNLDSKAVA	GSSGKVISGN	VSPSKGKMDE	TVNINAGNNI	EITRNGKNID	
H38	GWNLDSKAVA	GSSGKVISGN	VSPSKGKMDE	TVNINAGNNI	EITRNGKNID	
P20	GWNLDSKAVA	GSSGKVISGN	VSPSKGKMDE	TVNINAGNNI	EITRNGKNID	
Z2491	GWNLDSKAVA	GSSGKVISGN	VSPSKGKMDE	TVNINAGNNI	EISRNGKNID	
H41	GWNLDSKAVA	GSSGKVISGN	VSPSKGKMDE	TVNINAGNNI	EITRNGKNID	
Consensus	<u>GWNLDSKAVA</u>	<u>GSSGKVISGN</u>	<u>VSPSKGKMDE</u>	<u>TVNINAGNNI</u>	<u>EI-RNGKNID</u>	

C5

	451		500
EG327	IATSMTPQFS	SVSLGAGADA	PTLSVDDEGA LNVGSKDANK PVRITNVAPG
BZ198	IATSMAPQFS	SVSLGAGADA	PTLSVDDEGA LNVGSKDTNK PVRITNVAPG
BZ10	IATSMTPQFS	SVSLGAGADA	PTLSVDDEGA LNVGSKDANK PVRITNVAPG
H15	IATSMTPQFS	SVSLGAGADA	PTLSVDDEGA LNVGSKDANK PVRITNVAPG
EG329	IATSMTPQFS	SVSLGAGADA	PTLSVDG.DA LNVGSKKDNK PVRITNVAPG
PMC21	IATSMTPQFS	SVSLGAGADA	PTLSVDG.DA LNVGSKKDNK PVRITNVAPG
H38	IATSMTPQFS	SVSLGAGADA	PTLSVDDKGA LNVGSKDANK PVRITNVAPG
P20	IATSMTPQFS	SVSLGAGADA	PTLSVDDEGA LNVGSKDANK PVRITNVAPG
Z2491	IATSMAPQFS	SVSLGAGADA	PTLSVDDEGA LNVGSKDANK PVRITNVAPG
H41	IATSMTPQFS	SVSLGAGADA	PTLSVDDEGA LNVGSKDANK PVRITNVAPG
Consensus	<u>IATSM-POFS</u>	<u>SVSLGAGADA</u>	<u>PTLSVD---A LNVGSK--NK PVRITNVAPG</u>

C5

	501		550
EG327	VKEGDVTNVA	QLKGVAQNIN	NHIDNVDGNA RAGIAQAIAT AGLVQAYLPG
BZ198	VKEGDVTNVA	QLKGVAQNIN	NRIDNVDGNA RAGIAQAIAT AGLVQAYLPG
BZ10	VKEGDVTNVA	QLKGVAQNIN	NRIDNVDGNA RAGIAQAIAT AGLVQAYLPG
H15	VKEGDVTNVA	QLKGVAQNIN	NRIDNVDGNA RAGIAQAIAT AGLVQAYLPG
EG329	VKEGDVTNVA	QLKGVAQNIN	NRIDNVDGNA RAGIAQAIAT AGLVQAYLPG
PMC21	VKEGDVTNVA	QLKGVAQNIN	NRIDNVDGNA RAGIAQAIAT AGLVQAYLPG
H38	VKEGDVTNVA	QLKGVAQNIN	NRIDNVDGNA RAGIAQAIAT AGLVQAYLPG
P20	VKEGDVTNVA	QLKGVAQNIN	NRIDNVNGNA RAGIAQAIAT AGLVQAYLPG
Z2491	VKEGDVTNVA	QLKGVAQNIN	NRIDNVDGNA RAGIAQAIAT AGLVQAYLPG
H41	VKEGDVTNVA	QLKGVAQNIN	NRIDNVNGNA RAGIAQAIAT AGLVQAYLPG
Consensus	<u>VKEGDVTNVA</u>	<u>QLKGVAQNIN</u>	<u>N-IDNV-GNA RAGIAQAIAT AGL-QAYLPG</u>

C5

	551		600
EG327	KSMMAIGGGT	YRGEAGYAIG	YSSISDGGNW IIKGTASGNS RGHFGASASV
BZ198	KSMMAIGGGT	YRGEAGYAIG	YSSISDGGNW IIKGTASGNS RGHFGASASV
BZ10	KSMMAIGGGT	YRGEAGYAIG	YSSISDTGNW VIKGTASGNS RGHFGTSASV
H15	KSMMAIGGGT	YRGEAGYAIG	YSSISDTGNW VIKGTASGNS RGHFGTSASV
EG329	KSMMAIGGGT	YRGEAGYAIG	YSSISDGGNW IIKGTASGNS RGHFGASASV
PMC21	KSMMAIGGGT	YRGEAGYAIG	YSSISDGGNW IIKGTASGNS RGHFGASASV
H38	KSMMAIGGGT	YRGEAGYAIG	YSSISDGGNW IIKGTASGNS RGHFGASASV
P20	KSMMAIGGGT	YLGEAGYAIG	YSSISDTGNW VIKGTASGNS RGHFGTSASV
Z2491	KSMMAIGGGT	YRGEAGYAIG	YSSISDGGNW IIKGTASGNS RGHFGTSASV
H41	KSMMAIGGGT	YLGEAGYAIG	YSSISAGGNW IIKGTASGNS RGHFGASASV
Consensus	<u>KSMMAIGG-T</u>	<u>Y-GEAGYAIG</u>	<u>YSSIS--GNW -IKGTASGNS RGHFG-SASV</u>

C5

**FIG. 1 cont.**

601  
EG327 GYQW.  
BZ198 GYQW.  
BZ10 GYQW.  
H15 GYQW.  
EG329 GYQW.  
PMC21 GYQW.  
H38 GYQW.  
P20 GYQW.  
Z2491 GYQW.  
H41 GYQW.  
Consensus GYQW.  
C5

**FIG. 1 cont.**

1

H15	ATGAACAAAA	TATACCGCAT	CATTGGAAT	AGTGCCCTCA	ATGCCTGGGT	CGTCGTATCC	GAGCTCACAC	70
B210	ATGAACAAAA	TATCCCGCAT	CATTGGAAT	AGTGCCCTCA	ATGCCTGGGT	CGTCGTATCC	GAGCTCACAC	
B2198	ATGAACAAAA	TATACCGCAT	CATTGGAAT	AGTGCCCTCA	ATGCCTGGGT	CGTCGTATCC	GAGCTCACAC	
P20	ATGAACAAAA	TATACCGCAT	CATTGGAAT	AGTGCCCTCA	ATGCCTGGGT	CGTCGTATCC	GAGCTCACAC	
H38	ATGAACAAAA	TATACCGCAT	CATTGGAAT	AGTGCCCTCA	ATGCCTGGGT	CGTCGTATCC	GAGCTCACAC	
Z2491	ATGAACAAAA	TATACCGCAT	CATTGGAAT	AGTGCCCTCA	ATGCCTGGGT	CGTCGTATCC	GAGCTCACAC	
H41	ATGAACAAAA	TATACCGCAT	CATTGGAAT	AGTGCCCTCA	ATGCCTGGGT	CGTCGTATCC	GAGCTCACAC	
EG329	ATGAACGAAA	TATTGCGCAT	CATTGGAAT	AGTGCCCTCA	ATGCCTGGGT	CGTCGTATCC	GAGCTCACAC	
PMC21	ATGAACAAAA	TATACCGCAT	CATTGGAAT	AGTGCCCTCA	ATGCATGGGT	CGTCGTATCC	GAGCTCACAC	
EG327	ATGAACAAAA	TATACCGCAT	CATTGGAAT	AGTGCCCTCA	ATGCCTGGGT	CGTCGTATCC	GAGCTCACAC	
Consensus	ATGAAC-AAA	TAT--CGCAT	CATTGGAAT	AG-GCCCTCA	ATGC-TGGGT	-G--GTATCC	GAGCTCACAC	

C1

71

H15	GCAACCACAC	CAAACGCGCC	TCCGCAACCG	TGGCGACCGC	CGTATTGGCG	ACACTGTTGT	TTGCAACGGT	140
B210	GCAACCACAC	CAAACGCGCC	TCCGCAACCG	TGGCGACCGC	CGTATTGGCG	ACACTGTTGT	TTGCAACGGT	
B2198	GCAACCACAC	CAAACGCGCC	TCCGCAACCG	TGGCGACCGC	CGTATTGGCG	ACACTGTTGT	TTGCAACGGT	
P20	GCAACCACAC	CAAACGCGCC	TCCGCAACCG	TGGCGACCGC	CGTATTGGCG	ACACTGTTGT	TTGCAACGGT	
H38	GCAACCACAC	CAAACGCGCC	TCCGCAACCG	TGGCGACCGC	CGTATTGGCG	ACACTGTTGT	TTGCAACGGT	
Z2491	GCAACCACAC	CAAACGCGCC	TCCGCAACCG	TGAAGACCGC	CGTATTGGCG	ACACTGTTGT	TTGCAACGGT	
H41	GCAACCACAC	CAAACGCGCC	TCCGCAACCG	TGAAGACCGC	CGTATTGGCG	ACACTGTTGT	TTGCAACGGT	
EG329	GCAACCACAC	CAAACGCGCC	TCCGCAACCG	TGAAGACCGC	CGTATTGGCG	ACACTGTTGT	TTGCAACGGT	
PMC21	GCAACCACAC	CAAACGCGCC	TCCGCAACCG	TGAAGACCGC	CGTATTGGCG	ACTCTGTTGT	TTGCAACGGT	
EG327	GCAACCACAC	CAAACGCGCC	TCCGCAACCG	TGGCGACCGC	CGTATTGGCG	ACTCTGTTGT	TTGCAACGGT	
Consensus	GCAACCACAC	CAAACGCGCC	TCCGCAACCG	TG--GACCGC	CGTATTGGCG	AC-CTG-TGT	--GCAACGGT	

C1

141

H15	TCAGGCGAAT	GCTACCGATG	ACGAC.....	....GATTTA	TATTTAGAAC	CCGTACAACG	CACCTGCTGTC	210
B210	TCAGGCGAAT	GCTACCGATG	ACGAC.....	....GATTTA	TATTTAGAAC	CCGTACAACG	CACCTGCTGTC	
B2198	TCAGGCGAAT	GCTACCGATG	ACGAC.....	....GATTTA	TATTTAGAAC	CCGTACAACG	CACCTGCTGTC	
P20	TCAGGCGAAT	GCTACCGATA	CCGAT.....	....GAAGATGAA	GAGTTAGAA	CCGTAGCACG	CTCTGCTCTG	
H38	TCAGGCGAAT	GCTACCGATG	AAGAT.....	....GAAGAAGAA	GAGTTAGAA	CCGTAGTACG	CTCTGCTCTG	
Z2491	TCAGGCGAAT	GCTACCGATG	AAGAT.....	....GAAGAAGAA	GAGTTAGAA	CCGTACAACG	CTCTGCTCTG	
H41	TCAGGCGAAT	GCTACCGATG	AAGAT.....	....GAAGAAGAA	GAGTTAGAA	CCGTACAACG	CTCTGCTCTG	
EG329	TCAGGCAAGT	GCTAACCAATG	AAGAGCAAGA	AGAAGATTTA	TATTTAGACC	CCGTACAACG	CTCTGCTCTG	
PMC21	TCAGGCAAGT	GCTAACCAATG	AAGAGCAAGA	AGAAGATTTA	TATTTAGACC	CCGTACAACG	CTCTGCTCTG	
EG327	TCAGGCGAGT	ACTACCGATG	ACGAC.....	....GATTTA	TATTTAGAAC	CCGTACAACG	CACCTGCTGTC	
Consensus	TCAGGC-A-T	-CTA-C-AT-	--GA-----	----GA--A	-A-TTAGA--	CCGT---ACG	C-CTG----	

C1 V1

211

H15	GTGTTGAGCT	TCCGTTCCGA	TAAAGAAGGC	ACGGGAGAAA	AAGAAGGTAC	AGAAGA...T	TCAAATTGGG	280
B210	GTGTTGAGCT	TCCGTTCCGA	TAAAGAAGGC	ACGGGAGAAA	AAGAAGGTAC	AGAAGA...T	TCAAATTGGG	
B2198	GTGTTGAGCT	TCCGTTCCGA	TAAAGAAGGC	ACGGGAGAAA	AAGAAGGTAC	AGAAGA...T	TCAAATTGGG	
P20	GTGTTGCAAT	TCATGATCGA	TAAAGAAGGC	AATGGAGAAA	TCGAATCTAC	AGGAGA...T	ATAGGTTGGA	
H38	GTGTTGCAAT	TCATGATCGA	TAAAGAAGGC	AATGGAGAAA	ACGAATCTAC	AGGAAA...T	ATAGGTTGGA	
Z2491	GGG...AGCAT	TCAAG.CCAG	TATGGAAGGC	AGCGGCGAAT	TGGAAACGAT	ATCAT...T	ATCAATGACT	
H41	GTAGGGAGCA	TTCAAGCCAG	TATGGAAGGC	AGCGTCGAAT	TGGAAACGAT	A.....	TCATTATCAA	
EG329	GTGTTGATAG	TCAATTCCGA	TAAAGAAGGC	ACGGGAGAAA	AAGAAAAAGT	AGAAGAAAAT	TCAGATTGGG	
PMC21	GTGTTGATAG	TCAATTCCGA	TAAAGAAGGC	ACGGGAGAAA	AAGAAAAAGT	AGAAGAAAAT	TCAGATTGGG	
EG327	GTGTTGAGCT	TCCGTTCCGA	TAAAGAAGGC	ACGGGAGAAA	AAGAAGTTAC	AGAAGA...T	TCAAATTGGG	
Consensus	G-----	T-----C--	TA--GAAGGC	A--G--GAA-	--GAA----	A-----	-----	

V1

FIG. 2

	181								350
H15	CAGTATATT	CGACGAGAA	AGAGTACTAA	AAGCCGGAGC	AATCACCTTC	AAAGCCGGCG	ACAACCTGAA		
BZ10	CAGTATATT	CGACGAGAA	AGAGTACTAA	AAGCCGGAGC	AATCACCTTC	AAAGCCGGCG	ACAACCTGAA		
BZ198	CAGTATATT	CGACGAGAA	AGAGTACTAA	AAGCCGGAGC	AATCACCTTC	AAAGCCGGCG	ACAACCTGAA		
P20	GTATATATTA	CGACGATCAC	AACACTCTAC	ACGGCGCAAC	CGTTACCCTC	AAAGCCGGCG	ACAACCTGAA		
H38	GTATATATTA	CGACAATCAC	AACACTCTAC	ACGGCGCAAC	CGTTACCCTC	AAAGCCGGCG	ACAACCTGAA		
Z2491	AAGCAGCA	AGGAATTGT	AGACCCATA	ATAGTA....	.GTACCCTC	AAAGCCGGCG	ACAACCTGAA		
H41	TGACTAACGA	CAGCAAGGAA	TTTGTAGACC	TACATAGTT	AGTTACCTC	AAAGCCGGCG	ACAACCTGAA		
EG329	CAGTATATT	CAACGAGAAA	GGAGTACTAA	CAGCCAGAGA	AATCACCTTC	AAAGCCGGCG	ACAACCTGAA		
PMC21	CAGTATATT	CACGAGAAA	GGAGTACTAA	CAGCCAGAGA	AATCACCTTC	AAAGCCGGCG	ACAACCTGAA		
EG327	GAGTATATT	CGACAAGAAA	GGAGTACTAA	ACGCCGGAAC	AATCACCTTC	AAAGCCGGCG	ACAACCTGAA		
Consensus	-A-	-A-	-A-	-A-	-T-ACCCTC	AAAGCCGGCG	ACAACCTGAA		

**FIG. 2 cont.**

631  
H15 AACGACAAC TTACCGATGA CGAGAAAAA CGTGCGGCAA GCGTTAAAGA CGTATTAAAC GCAGGCTGGA 700  
B210 AACGACAACG TTACCGATGA CGAGAAAAA CGTGCGGCAA GCGTTAAAGA CGTATTAAAC GCAGGCTGGA  
B2198 AACGACAACG TTACCGATGA CGAGAAAAA CGTGCGGCAA GCGTTAAAGA CGTATTAAAC GCAGGCTGGA  
P20 GGTAAACAAA GTACACATTA C.....ACT CGTGCGGCAA GTATTAAAGA TGTGTTGAAT GCGGGTTGGA  
H38 AACGACAACG TTACCGATGA CAAGAAAAA CGTGCGGCAA GCGTTAAAGA CGTATTAAAC GCAGGCTGGA  
Z2491 GGTAAACAAA GTACACATTA C.....ACT CGTGCGGCAA GTATTAAAGA TGTGTTGAAT GCGGGTTGGA  
H41 AACGACAACG TTACCGATGA CGAGAAAAA CGTGCGGCAA GCGTTAAAGA CGTATTAAAC GCAGGCTGGA  
EG329 AACGACAACG TTACCGATGA CGAGAAAAA CGTGCGGCAA GCGTTAAAGA CGTATTAAAC GCAGGCTGGA  
PMC21 AACGACAACG TTACCGATGA CGAGAAAAA CGTGCGGCAA GCGTTAAAGA CGTATTAAAC GCAGGCTGGA  
EG327 AACGACAACG TTACCGATGA CGAGAAAAA CGTGCGGCAA GCGTTAAAGA CGTATTAAAC GCAGGCTGGA  
Consensus ----AC-A-- -TAC--AT-A C-----A-- CGTGC-GCAA G--TTAA-GA -GT-TT-AA GC-GG-TGGA

V3

C4

701  
H15 ACATTAAAGG CGTTAAACCC GGTACAACAG CT.....TC CGATAACGTT GATTTCGTCC GCACCTACGA 770  
B210 ACATTAAAGG CGTTAAACCC GGTACAACAG CT.....TC CGATAACGTT GATTTCGTCC GCACCTACGA  
B2198 ACATTAAAGG CGTTAAACCC GGTACAACAG CT.....TC CGATAACGTT GATTTCGTCC GCACCTACGA  
P20 ATATTAAAGG TGTAAACT GGTCAACAA CTGGTCAATC AGAAATGTC GATTTCGTCC GCACCTACGA  
H38 ACATTAAAGG CGTTAAACCC GGTACAACAG CT.....TC CGATAACGTT GATTTCGTCC GCACCTACGA  
Z2491 ATATTAAAGG TGTAAACT GGTCAACAA CTGGTCAATC AGAAATGTC GATTTCGTCC GCACCTACGA  
H41 ACATTAAAGG CGTTAAACCC GGTACAACAG CT.....TC CGATAACGTT GATTTCGTCC GCACCTACGA  
EG329 ACATTAAAGG CGTTAAACCC GGTACAACAG CT.....TC CGATAACGTT GATTTCGTCC GCACCTACGA  
PMC21 ACATTAAAGG CGTTAAACCC GGTACAACAG CT.....TC CGATAACGTT GATTTCGTCC GCACCTACGA  
EG327 ACATTAAAGG CGTTAAACCC GGTACAACAG CT.....TC CGATAACGTT GATTTCGTCC GCACCTACGA  
Consensus A-ATTAA-GG -GTTAA-C- GG--CAACA- CT-----TC -GA-AA-GT- GATTTCGTCC -GACTTACGA

C4

V4

C5

771  
H15 CACAGTCGAG TTCTTGAGCG CAGATACGAA AACACGACT GTTAATGTGG AAAGCAAAGA CAACGGCAAG 840  
B210 CACAGTCGAG TTCTTGAGCG CAGATACGAA AACACGACT GTTAATGTGG AAAGCAAAGA CAACGGCAAG  
B2198 CACAGTCGAG TTCTTGAGCG CAGATACGAA AACACGACT GTTAATGTGG AAAGCAAAGA CAACGGCAAG  
P20 CACAGTCGAG TTCTTGAGCG CAGATACGAA AACACGACT GTTAATGTGG AAAGCAAAGA CAACGGCAAG  
H38 CACAGTCGAG TTCTTGAGCG CAGATACGAA AACACGACT GTTAATGTGG AAAGCAAAGA CAACGGCAAG  
Z2491 CACAGTCGAG TTCTTGAGCG CAGATACGAA AACACGACT GTTAATGTGG AAAGCAAAGA CAACGGCAAG  
H41 CACAGTCGAG TTCTTGAGCG CAGATACGAA AACACGACT GTTAATGTGG AAAGCAAAGA CAACGGCAAG  
EG329 CACAGTCGAG TTCTTGAGCG CAGATACGAA AACACGACT GTTAATGTGG AAAGCAAAGA CAACGGCAAG  
PMC21 CACAGTCGAG TTCTTGAGCG CAGATACGAA AACACGACT GTTAATGTGG AAAGCAAAGA CAACGGCAAG  
EG327 CACAGTCGAG TTCTTGAGCG CAGATACGAA AACACGACT GTTAATGTGG AAAGCAAAGA CAACGGCAAG  
Consensus CACAGTCGAG TTCTTGAGCG CAGATACGAA AACACGACT GTTAATGTGG AAAGCAAAGA CAACGGCAAG

C5

841  
H15 AAAACCGAAG TTAATAATCGG TGCGAAGACT TCTGTTATTA AAGAAAAAGA CGGTAAGTTG GTTACTGGTA 910  
B210 AAAACCGAAG TTAATAATCGG TGCGAAGACT TCTGTTATTA AAGAAAAAGA CGGTAAGTTG GTTACTGGTA  
B2198 AAAACCGAAG TTAATAATCGG TGCGAAGACT TCTGTTATTA AAGAAAAAGA CGGTAAGTTG GTTACTGGTA  
P20 AAAACCGAAG TTAATAATCGG TGCGAAGACT TCTGTTATTA AAGAAAAAGA CGGTAAGTTG GTTACTGGTA  
H38 AAAACCGAAG TTAATAATCGG TGCGAAGACT TCTGTTATTA AAGAAAAAGA CGGTAAGTTG GTTACTGGTA  
Z2491 AAAACCGAAG TTAATAATCGG TGCGAAGACT TCTGTTATTA AAGAAAAAGA CGGTAAGTTG GTTACTGGTA  
H41 AAAACCGAAG TTAATAATCGG TGCGAAGACT TCTGTTATTA AAGAAAAAGA CGGTAAGTTG GTTACTGGTA  
EG329 AAAACCGAAG TTAATAATCGG TGCGAAGACT TCTGTTATTA AAGAAAAAGA CGGTAAGTTG GTTACTGGTA  
PMC21 AAAACCGAAG TTAATAATCGG TGCGAAGACT TCTGTTATTA AAGAAAAAGA CGGTAAGTTG GTTACTGGTA  
EG327 AAAACCGAAG TTAATAATCGG TGCGAAGACT TCTGTTATTA AAGAAAAAGA CGGTAAGTTG GTTACTGGTA  
Consensus A-AAACCGAAG TTAATAATCGG TGCGAAGACT TCTGTTATTA AAGAAAAAGA CGGTAAGTTG GTTACTGGTA

C5

911  
H15 AAGGCAAAG CGAGAATGGT TCTTCTACAG ACGAAGGCGA AGGCTTAGTG ACTGCAAAG AAGTGATTGA 980  
B210 AAGGCAAAG CGAGAATGGT TCTTCTACAG ACGAAGGCGA AGGCTTAGTG ACTGCAAAG AAGTGATTGA  
B2198 AAGGCAAAG CGAGAATGGT TCTTCTACAG ACGAAGGCGA AGGCTTAGTG ACTGCAAAG AAGTGATTGA  
P20 AAGGCAAAG CGAGAATGGT TCTTCTACAG ACGAAGGCGA AGGCTTAGTG ACTGCAAAG AAGTGATTGA  
H38 AAGGCAAAG CGAGAATGGT TCTTCTACAG ACGAAGGCGA AGGCTTAGTG ACTGCAAAG AAGTGATTGA  
Z2491 AAGGCAAAG CGAGAATGGT TCTTCTACAG ACGAAGGCGA AGGCTTAGTG ACTGCAAAG AAGTGATTGA  
H41 AAGGCAAAG CGAGAATGGT TCTTCTACAG ACGAAGGCGA AGGCTTAGTG ACTGCAAAG AAGTGATTGA  
EG329 AAGGCAAAG CGAGAATGGT TCTTCTACAG ACGAAGGCGA AGGCTTAGTG ACTGCAAAG AAGTGATTGA  
PMC21 AAGGCAAAG CGAGAATGGT TCTTCTACAG ACGAAGGCGA AGGCTTAGTG ACTGCAAAG AAGTGATTGA  
EG327 AAGGCAAAG CGAGAATGGT TCTTCTACAG ACGAAGGCGA AGGCTTAGTG ACTGCAAAG AAGTGATTGA  
Consensus AAG-CAAG- CGAGAATG-T TCTTCTACAG AC-AAGGCGA AGGCTTAGTG ACTGCAAAG AAGTGATTGA

C5

FIG. 2 cont.

981 1050

H15	TGCAGTAAAC	AAGGCTGGTT	GGAGATGAA	AACAACAACC	GCTAATGGTC	AAACAGGTCA	AGCTGACAAG
B210	TGCAGTAAAC	AAGGCTGGTT	GGAGATGAA	AACAACAACC	GCTAATGGTC	AAACAGGTCA	AGCTGACAAG
BZ198	TGCAGTAAAC	AAGGCTGGTT	GGAGATGAA	AACAACAACC	GCTAATGGTC	AAACAGGTCA	AGCTGACAAG
P20	TGCAGTAAAC	AAGGCTGGTT	GGAGATGAA	AACAACAACC	GCTAATGGTC	AAACAGGTCA	AGCTGACAAG
H38	TGCAGTAAAC	AAGGCTGGTT	GGAGATGAA	AACAACAACC	GCTAATGGTC	AAACAGGTCA	AGCTGACAAG
Z2491	TGCAGTAAAC	AAGGCTGGTT	GGAGATGAA	AACAACAACC	GCTAATGGTC	AAACAGGTCA	AGCTGACAAG
H41	TGCAGTAAAC	AAGGCTGGTT	GGAGATGAA	AACAACAACC	GCTAATGGTC	AAACAGGTCA	AGCTGACAAG
EG329	TGCAGTAAAC	AAGGCTGGTT	GGAGATGAA	AACAACAACC	GCTAATGGTC	AAACAGGTCA	AGCTGACAAG
PMC21	TGCAGTAAAC	AAGGCTGGTT	GGAGATGAA	AACAACAACC	GCTAATGGTC	AAACAGGTCA	AGCTGACAAG
EG327	TGCAGTAAAC	AAGGCTGGTT	GGAGATGAA	AACAACAACC	GCTAATGGTC	AAACAGGTCA	AGCTGACAAG
Consensus	TGCAGTAAAC	AAGGCTGGTT	GGAGATGAA	AACAACAACC	GCTAATGGTC	AAACAGGTCA	AGCTGACAAG

C5

1051 1120

H15	TTTGAACCG	TTACATCAGG	CACAAAAGTA	ACCTTTGCTA	GTGGTAATGG	TACAACCTCGG	ACTGTAAGTA
B210	TTTGAACCG	TTACATCAGG	CACAAAAGTA	ACCTTTGCTA	GTGGTAATGG	TACAACCTCGG	ACTGTAAGTA
BZ198	TTTGAACCG	TTACATCAGG	CACAAAAGTA	ACCTTTGCTA	GTGGTAATGG	TACAACCTCGG	ACTGTAAGTA
P20	TTTGAACCG	TTACATCAGG	CACAAAAGTA	ACCTTTGCTA	GTGGTAATGG	TACAACCTCGG	ACTGTAAGTA
H38	TTTGAACCG	TTACATCAGG	CACAAAAGTA	ACCTTTGCTA	GTGGTAATGG	TACAACCTCGG	ACTGTAAGTA
Z2491	TTTGAACCG	TTACATCAGG	CACAAAAGTA	ACCTTTGCTA	GTGGTAATGG	TACAACCTCGG	ACTGTAAGTA
H41	TTTGAACCG	TTACATCAGG	CACAAAAGTA	ACCTTTGCTA	GTGGTAATGG	TACAACCTCGG	ACTGTAAGTA
EG329	TTTGAACCG	TTACATCAGG	CACAAAAGTA	ACCTTTGCTA	GTGGTAATGG	TACAACCTCGG	ACTGTAAGTA
PMC21	TTTGAACCG	TTACATCAGG	CACAAAAGTA	ACCTTTGCTA	GTGGTAATGG	TACAACCTCGG	ACTGTAAGTA
EG327	TTTGAACCG	TTACATCAGG	CACAAAAGTA	ACCTTTGCTA	GTGGTAATGG	TACAACCTCGG	ACTGTAAGTA
Consensus	TTTGAACCG	TTACATCAGG	CACAAAAGTA	ACCTTTGCTA	GTGGTAATGG	TACAACCTCGG	ACTGTAAGTA

C5

1121 1190

H15	AAGATGATCA	AGGCAACATC	ACTGTTAAGT	ATGATGTAAA	TGTCGGCGAT	GCCCTAAACG	TCAATCAGCT
B210	AAGATGATCA	AGGCAACATC	ACTGTTAAGT	ATGATGTAAA	TGTCGGCGAT	GCCCTAAACG	TCAATCAGCT
BZ198	AAGATGATCA	AGGCAACATC	ACTGTTAAGT	ATGATGTAAA	TGTCGGCGAT	GCCCTAAACG	TCAATCAGCT
P20	AAGATGATCA	AGGCAACATC	ACTGTTAAGT	ATGATGTAAA	TGTCGGCGAT	GCCCTAAACG	TCAATCAGCT
H38	AAGATGATCA	AGGCAACATC	ACTGTTAAGT	ATGATGTAAA	TGTCGGCGAT	GCCCTAAACG	TCAATCAGCT
Z2491	AAGATGATCA	AGGCAACATC	ACTGTTAAGT	ATGATGTAAA	TGTCGGCGAT	GCCCTAAACG	TCAATCAGCT
H41	AAGATGATCA	AGGCAACATC	ACTGTTAAGT	ATGATGTAAA	TGTCGGCGAT	GCCCTAAACG	TCAATCAGCT
EG329	AAGATGATCA	AGGCAACATC	ACTGTTAAGT	ATGATGTAAA	TGTCGGCGAT	GCCCTAAACG	TCAATCAGCT
PMC21	AAGATGATCA	AGGCAACATC	ACTGTTAAGT	ATGATGTAAA	TGTCGGCGAT	GCCCTAAACG	TCAATCAGCT
EG327	AAGATGATCA	AGGCAACATC	ACTGTTAAGT	ATGATGTAAA	TGTCGGCGAT	GCCCTAAACG	TCAATCAGCT
Consensus	AAGATGATCA	AGGCAACATC	ACTGTTAAGT	ATGATGTAAA	TGTCGGCGAT	GCCCTAAACG	TCAATCAGCT

C5

1191 1260

H15	GCAAAACAGC	GGTTGGAATT	TGGATTCCAA	AGCGGTTGCA	GGTTCTTCGG	GCAAAGTCAT	CAGCGGCAAT
B210	GCAAAACAGC	GGTTGGAATT	TGGATTCCAA	AGCGGTTGCA	GGTTCTTCGG	GCAAAGTCAT	CAGCGGCAAT
BZ198	GCAAAACAGC	GGTTGGAATT	TGGATTCCAA	AGCGGTTGCA	GGTTCTTCGG	GCAAAGTCAT	CAGCGGCAAT
P20	GCAAAACAGC	GGTTGGAATT	TGGATTCCAA	AGCGGTTGCA	GGTTCTTCGG	GCAAAGTCAT	CAGCGGCAAT
H38	GCAAAACAGC	GGTTGGAATT	TGGATTCCAA	AGCGGTTGCA	GGTTCTTCGG	GCAAAGTCAT	CAGCGGCAAT
Z2491	GCAAAACAGC	GGTTGGAATT	TGGATTCCAA	AGCGGTTGCA	GGTTCTTCGG	GCAAAGTCAT	CAGCGGCAAT
H41	GCAAAACAGC	GGTTGGAATT	TGGATTCCAA	AGCGGTTGCA	GGTTCTTCGG	GCAAAGTCAT	CAGCGGCAAT
EG329	GCAAAACAGC	GGTTGGAATT	TGGATTCCAA	AGCGGTTGCA	GGTTCTTCGG	GCAAAGTCAT	CAGCGGCAAT
PMC21	GCAAAACAGC	GGTTGGAATT	TGGATTCCAA	AGCGGTTGCA	GGTTCTTCGG	GCAAAGTCAT	CAGCGGCAAT
EG327	GCAAAACAGC	GGTTGGAATT	TGGATTCCAA	AGCGGTTGCA	GGTTCTTCGG	GCAAAGTCAT	CAGCGGCAAT
Consensus	GCAAAACAGC	GGTTGGAATT	TGGATTCCAA	AGCGGTTGCA	GGTTCTTCGG	GCAAAGTCAT	CAGCGGCAAT

C5

1261 1330

H15	GTTTCGCCGA	GCAAGGGAAA	GATGGATGAA	ACCGTCAACA	TTAATGCCGG	CAACAACATC	GAGATTACCC
B210	GTTTCGCCGA	GCAAGGGAAA	GATGGATGAA	ACCGTCAACA	TTAATGCCGG	CAACAACATC	GAGATTACCC
BZ198	GTTTCGCCGA	GCAAGGGAAA	GATGGATGAA	ACCGTCAACA	TTAATGCCGG	CAACAACATC	GAGATTACCC
P20	GTTTCGCCGA	GCAAGGGAAA	GATGGATGAA	ACCGTCAACA	TTAATGCCGG	CAACAACATC	GAGATTACCC
H38	GTTTCGCCGA	GCAAGGGAAA	GATGGATGAA	ACCGTCAACA	TTAATGCCGG	CAACAACATC	GAGATTACCC
Z2491	GTTTCGCCGA	GCAAGGGAAA	GATGGATGAA	ACCGTCAACA	TTAATGCCGG	CAACAACATC	GAGATTACCC
H41	GTTTCGCCGA	GCAAGGGAAA	GATGGATGAA	ACCGTCAACA	TTAATGCCGG	CAACAACATC	GAGATTACCC
EG329	GTTTCGCCGA	GCAAGGGAAA	GATGGATGAA	ACCGTCAACA	TTAATGCCGG	CAACAACATC	GAGATTACCC
PMC21	GTTTCGCCGA	GCAAGGGAAA	GATGGATGAA	ACCGTCAACA	TTAATGCCGG	CAACAACATC	GAGATTACCC
EG327	GTTTCGCCGA	GCAAGGGAAA	GATGGATGAA	ACCGTCAACA	TTAATGCCGG	CAACAACATC	GAGATTACCC
Consensus	GTTTCGCCGA	GCAAGGGAAA	GATGGATGAA	ACCGTCAACA	TTAATGCCGG	CAACAACATC	GAGATTACCC

C5

FIG. 2 cont.



1331  
H15 GCAACGGCAA AAATATCGAC ATCGCCACTT CGATGACCCC GCAATTTTCC AGCGTTTCGC TCGGCGCGGG 1400  
B210 GCAACGGCAA AAATATCGAC ATCGCCACTT CGATGACCCC GCAATTTTCC AGCGTTTCGC TCGGCGCGGG  
B2198 GCAACGGTAA AAATATCGAC ATCGCCACTT CGATGACCCC GCAATTTTCC AGCGTTTCGC TCGGCGCGGG  
P20 GCAACGGCAA AAATATCGAC ATCGCCACTT CGATGACCCC GCAATTTTCC AGCGTTTCGC TCGGCGCGGG  
H38 GCAACGGTAA AAATATCGAC ATCGCCACTT CGATGACCCC GCAATTTTCC AGCGTTTCGC TCGGCGCGGG  
Z2491 GCAACGGTAA AAATATCGAC ATCGCCACTT CGATGACCCC GCAATTTTCC AGCGTTTCGC TCGGCGCGGG  
H41 GCAACGGCAA AAATATCGAC ATCGCCACTT CGATGACCCC GCAATTTTCC AGCGTTTCGC TCGGCGCGGG  
EG329 GCAACGGTAA AAATATCGAC ATCGCCACTT CGATGACCCC GCAATTTTCC AGCGTTTCGC TCGGCGCGGG  
PMC21 GCAACGGTAA AAATATCGAC ATCGCCACTT CGATGACCCC GCAATTTTCC AGCGTTTCGC TCGGCGCGGG  
EG327 GCAACGGCAA AAATATCGAC ATCGCCACTT CGATGACCCC GCAATTTTCC AGCGTTTCGC TCGGCGCGGG  
Consensus GCAACGG-AA AAATATCGAC ATCGCCACTT CGATG-C-CC GCA-TTTTCC AGCGTTTCGC TCGG-CGCGG

C5

1401  
H15 GCGCGATGCG CCCACTTTAA GCGTGGATGA CGAGGGCGCG TTGAATGTCTG GCAGCAAGGA TGCCAACAAA 1470  
B210 GCGCGATGCG CCCACTTTAA GCGTGGATGA CGAGGGCGCG TTGAATGTCTG GCAGCAAGGA TGCCAACAAA  
B2198 GCGCGATGCG CCCACTTTAA GCGTGGATGA CGAGGGCGCG TTGAATGTCTG GCAGCAAGGA TGCCAACAAA  
P20 GCGCGATGCG CCCACTTTAA GCGTGGATGA CGAGGGCGCG TTGAATGTCTG GCAGCAAGGA TGCCAACAAA  
H38 GCGCGATGCG CCCACTTTAA GCGTGGATGA CGAGGGCGCG TTGAATGTCTG GCAGCAAGGA TGCCAACAAA  
Z2491 GCGCGATGCG CCCACTTTAA GCGTGGATGA CGAGGGCGCG TTGAATGTCTG GCAGCAAGGA TGCCAACAAA  
H41 GCGCGATGCG CCCACTTTAA GCGTGGATGA CGAGGGCGCG TTGAATGTCTG GCAGCAAGGA TGCCAACAAA  
EG329 GCGCGATGCG CCCACTTTAA GCGTGGAT... .GCGGACGCA TTGAATGTCTG GCAGCAAGGA TGCCAACAAA  
PMC21 GCGCGATGCG CCCACTTTAA GCGTGGAT... .GCGGACGCA TTGAATGTCTG GCAGCAAGGA TGCCAACAAA  
EG327 GCGCGATGCG CCCACTTTAA GCGTGGATGA CGAGGGCGCG TTGAATGTCTG GCAGCAAGGA TGCCAACAAA  
Consensus GCG-GATGCG CCCACTTT-A GCGTGGAT-- ---GG-CGC- TTGAATGTCTG GCAGCAAG-A ---CAACAAA

C5

1471  
H15 CCGGTCCGCA TTACCAATGT CGCCCCGGGC GTTAAAGAGG GGGATGTTAC AAACGTCGCA CAACTTAAAG 1540  
B210 CCGGTCCGCA TTACCAATGT CGCCCCGGGC GTTAAAGAGG GGGATGTTAC AAACGTCGCA CAACTTAAAG  
B2198 CCGGTCCGCA TTACCAATGT CGCCCCGGGC GTTAAAGAGG GGGATGTTAC AAACGTCGCA CAACTTAAAG  
P20 CCGGTCCGCA TTACCAATGT CGCCCCGGGC GTTAAAGAGG GGGATGTTAC AAACGTCGCA CAACTTAAAG  
H38 CCGGTCCGCA TTACCAATGT CGCCCCGGGC GTTAAAGAGG GGGATGTTAC AAACGTCGCA CAACTTAAAG  
Z2491 CCGGTCCGCA TTACCAATGT CGCCCCGGGC GTTAAAGAGG GGGATGTTAC AAACGTCGCA CAACTTAAAG  
H41 CCGGTCCGCA TTACCAATGT CGCCCCGGGC GTTAAAGAGG GGGATGTTAC AAACGTCGCA CAACTTAAAG  
EG329 CCGGTCCGCA TTACCAATGT CGCCCCGGGC GTTAAAGAGG GGGATGTTAC AAACGTCGCA CAACTTAAAG  
PMC21 CCGGTCCGCA TTACCAATGT CGCCCCGGGC GTTAAAGAGG GGGATGTTAC AAACGTCGCA CAACTTAAAG  
EG327 CCGGTCCGCA TTACCAATGT CGCCCCGGGC GTTAAAGAGG GGGATGTTAC AAACGTCGCA CAACTTAAAG  
Consensus CCGGTCCGCA TTACCAATGT CGCCCCGGGC GTTAAAGAGG GGGATGTTAC AAACGTCGC- CAACTTAAAG

C5

1541  
H15 GTGTGGCGCA AAACCTGAAC AACCGCATCG ACAATGTGGA CGGCAACGCG CGTGGCGGTA TCGCCCAAGC 1610  
B210 GTGTGGCGCA AAACCTGAAC AACCGCATCG ACAATGTGGA CGGCAACGCG CGTGGCGGTA TCGCCCAAGC  
B2198 GTGTGGCGCA AAACCTGAAC AACCGCATCG ACAATGTGGA CGGCAACGCG CGTGGCGGTA TCGCCCAAGC  
P20 GTGTGGCGCA AAACCTGAAC AACCGCATCG ACAATGTGGA CGGCAACGCG CGTGGCGGTA TCGCCCAAGC  
H38 GTGTGGCGCA AAACCTGAAC AACCGCATCG ACAATGTGGA CGGCAACGCG CGTGGCGGTA TCGCCCAAGC  
Z2491 GTGTGGCGCA AAACCTGAAC AACCGCATCG ACAATGTGGA CGGCAACGCG CGTGGCGGTA TCGCCCAAGC  
H41 GTGTGGCGCA AAACCTGAAC AACCGCATCG ACAATGTGGA CGGCAACGCG CGTGGCGGTA TCGCCCAAGC  
EG329 GTGTGGCGCA AAACCTGAAC AACCGCATCG ACAATGTGGA CGGCAACGCG CGTGGCGGTA TCGCCCAAGC  
PMC21 GTGTGGCGCA AAACCTGAAC AACCGCATCG ACAATGTGGA CGGCAACGCG CGTGGCGGTA TCGCCCAAGC  
EG327 GTGTGGCGCA AAACCTGAAC AACCGCATCG ACAATGTGGA CGGCAACGCG CGTGGCGGTA TCGCCCAAGC  
Consensus G-GTGGCGCA AAACCTGAAC AACCGCATCG ACAATGTGGA CGGCAACGCG CG-GCGG-A TCGCCCAAGC

C5

1611  
H15 GATTGCAACC GCAGGTTTGG CTCAGGCGTA TTTGCCCGGC AAGAGTATGA TGGCGATCGG CGGCGGTACT 1680  
B210 GATTGCAACC GCAGGTTTGG CTCAGGCGTA TTTGCCCGGC AAGAGTATGA TGGCGATCGG CGGCGGTACT  
B2198 GATTGCAACC GCAGGTTTGG CTCAGGCGTA TTTGCCCGGC AAGAGTATGA TGGCGATCGG CGGCGGTACT  
P20 GATTGCAACC GCAGGTTTGG CTCAGGCGTA TTTGCCCGGC AAGAGTATGA TGGCGATCGG CGGCGGTACT  
H38 GATTGCAACC GCAGGTTTGG CTCAGGCGTA TTTGCCCGGC AAGAGTATGA TGGCGATCGG CGGCGGTACT  
Z2491 GATTGCAACC GCAGGTTTGG CTCAGGCGTA TTTGCCCGGC AAGAGTATGA TGGCGATCGG CGGCGGTACT  
H41 GATTGCAACC GCAGGTTTGG CTCAGGCGTA TTTGCCCGGC AAGAGTATGA TGGCGATCGG CGGCGGTACT  
EG329 GATTGCAACC GCAGGTTTGG CTCAGGCGTA TTTGCCCGGC AAGAGTATGA TGGCGATCGG CGGCGGTACT  
PMC21 GATTGCAACC GCAGGTTTGG CTCAGGCGTA TTTGCCCGGC AAGAGTATGA TGGCGATCGG CGGCGGTACT  
EG327 GATTGCAACC GCAGGTTTGG CTCAGGCGTA TTTGCCCGGC AAGAGTATGA TGGCGATCGG CGGCGGTACT  
Consensus GATTGCAACC GCAGG-T-G -TCAGGCG-TA T-TGCCCGGC AAGAGTATGA TGGCGATCGG CGGCG--ACT

C5

FIG. 2 cont.

1681

H15	TATCGCGGCG	AAGCCGGTTA	CGCCATCGGC	TACTCGAGCA	TTTCTGACAC	TGGGAATTGG	GTTATCAAGG	1750
BZ10	TATCGCGGCG	AAGCCGGTTA	CGCCATCGGC	TACTCGAGCA	TTTCTGACAC	TGGGAATTGG	GTTATCAAGG	
BZ198	TATCGCGGCG	AAGCCGGTTA	CGCCATCGGC	TACTCAAGTA	TTTCCGACGG	CGGAAATTGG	ATTATCAAAG	
P20	TATCTCGGCG	AAGCCGGTTA	CGCCATCGGC	TACTCGAGCA	TTTCTGACAC	TGGGAATTGG	GTTATCAAGG	
H38	TATCGCGGCG	AAGCCGGTTA	CGCCATCGGC	TACTCCAGTA	TTTCCGACGG	CGGAAATTGG	ATTATCAAAG	
Z2491	TATCGCGGCG	AAGCCGGTTA	CGCCATCGGC	TACTCCAGTA	TTTCCGACGG	CGGAAATTGG	ATTATCAAAG	
H41	TATCTCGGCG	AAGCCGGTTA	TGCCATCGGC	TACTCAAGCA	TTTCCGACGG	CGGAAATTGG	ATTATCAAAG	
EG329	TATCGCGGCG	AAGCCGGTTA	CGCCATCGGC	TACTCCAGTA	TTTCCGACGG	CGGAAATTGG	ATTATCAAAG	
PMC21	TATCGCGGCG	AAGCCGGTTA	CGCCATCGGC	TACTCCAGTA	TTTCCGACGG	CGGAAATTGG	ATTATCAAAG	
EG327	TATCGCGGCG	AAGCCGGTTA	TGCCATCGGC	TACTCAAGCA	TTTCCGACGG	CGGAAATTGG	ATTATCAAAG	
Consensus	<u>TATC-CGGCG</u>	<u>AAGCCGGTTA</u>	<u>-GCCATCGGC</u>	<u>TACTC-AG-A</u>	<u>TTTC-G-C--</u>	<u>-GG-AATTGG</u>	<u>-TTATCAA-G</u>	

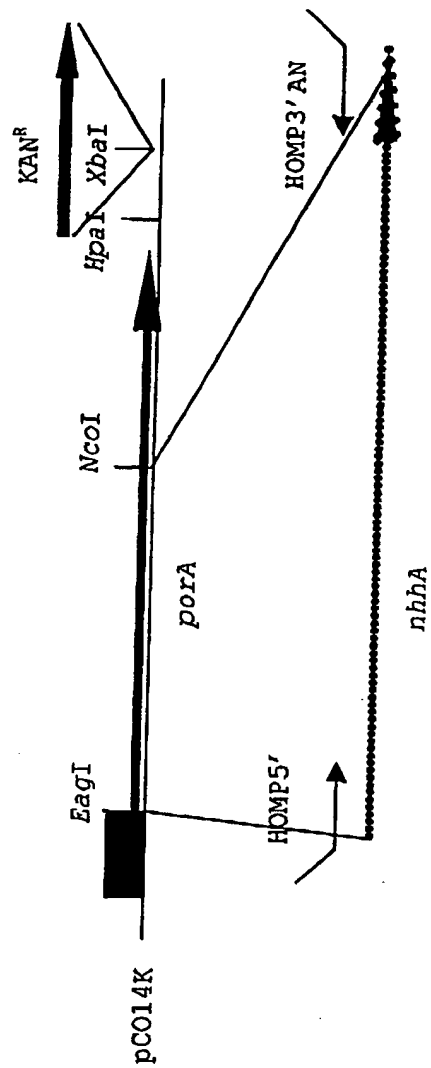
C5

1751

H15	GCACGGCTTC	CGGCAATTTCG	CGCGGCCATT	TCGGTGCTTC	CGCATCTGTC	GGTTATCAGT	GGTAA	1815
BZ10	GCACGGCTTC	CGGCAATTTCG	CGCGGTCATT	TCGGTACTTC	CGCATCTGTC	GGTTATCAGT	GGTAA	
BZ198	GCACGGCTTC	CGGCAATTTCG	CGCGGCCATT	TCGGTGCTTC	CGCATCTGTC	GGTTATCAAT	GGTAA	
P20	GCACGGCTTC	CGGCAATTTCG	CGCGGTCATT	TCGGTACTTC	CGCATCTGTC	GGTTATCAGT	GGTAA	
H38	GCACGGCTTC	CGGCAATTTCG	CGCGGTCATT	TCGGTGCTTC	CGCATCTGTC	GGTTATCAGT	GGTAA	
Z2491	GCACGGCTTC	CGGCAATTTCG	CGCGGCCATT	TCGGTGCTTC	CGCATCTGTC	GGTTATCAGT	GGTAA	
H41	GCACGGCTTC	CGGCAATTTCG	CGCGGCCATT	TCGGTGCTTC	CGCATCTGTC	GGTTATCAGT	GGTAA	
EG329	GCACGGCTTC	CGGCAATTTCG	CGCGGCCATT	TCGGTGCTTC	CGCATCTGTC	GGTTATCAGT	GGTAA	
PMC21	GCACGGCTTC	CGGCAATTTCG	CGCGGCCATT	TCGGTGCTTC	CGCATCTGTC	GGTTATCAGT	GGTAA	
EG327	GCACGGCTTC	CGGCAATTTCG	CGCGGCCATT	TCGGTGCTTC	CGCATCTGTC	GGTTATCAGT	GGTAA	
Consensus	<u>GCACGGCTTC</u>	<u>CGGCAATTTCG</u>	<u>CGCGG-CATT</u>	<u>TCGGT-CTTC</u>	<u>CGCATCTGTC</u>	<u>GGTTATCA-T</u>	<u>GGTAA</u>	

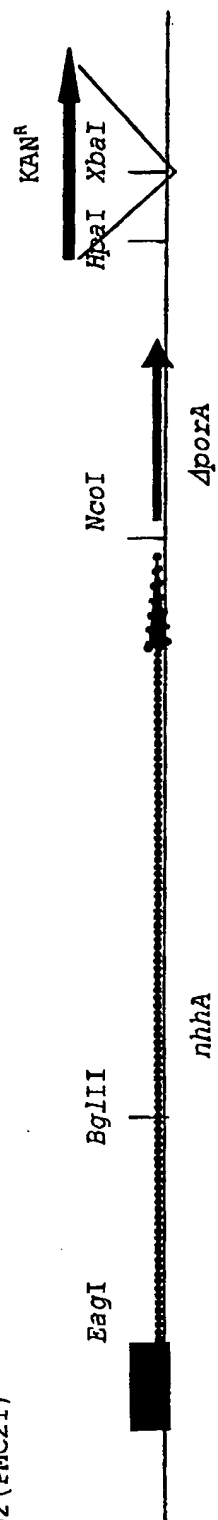
C5

**FIG. 2 cont.**

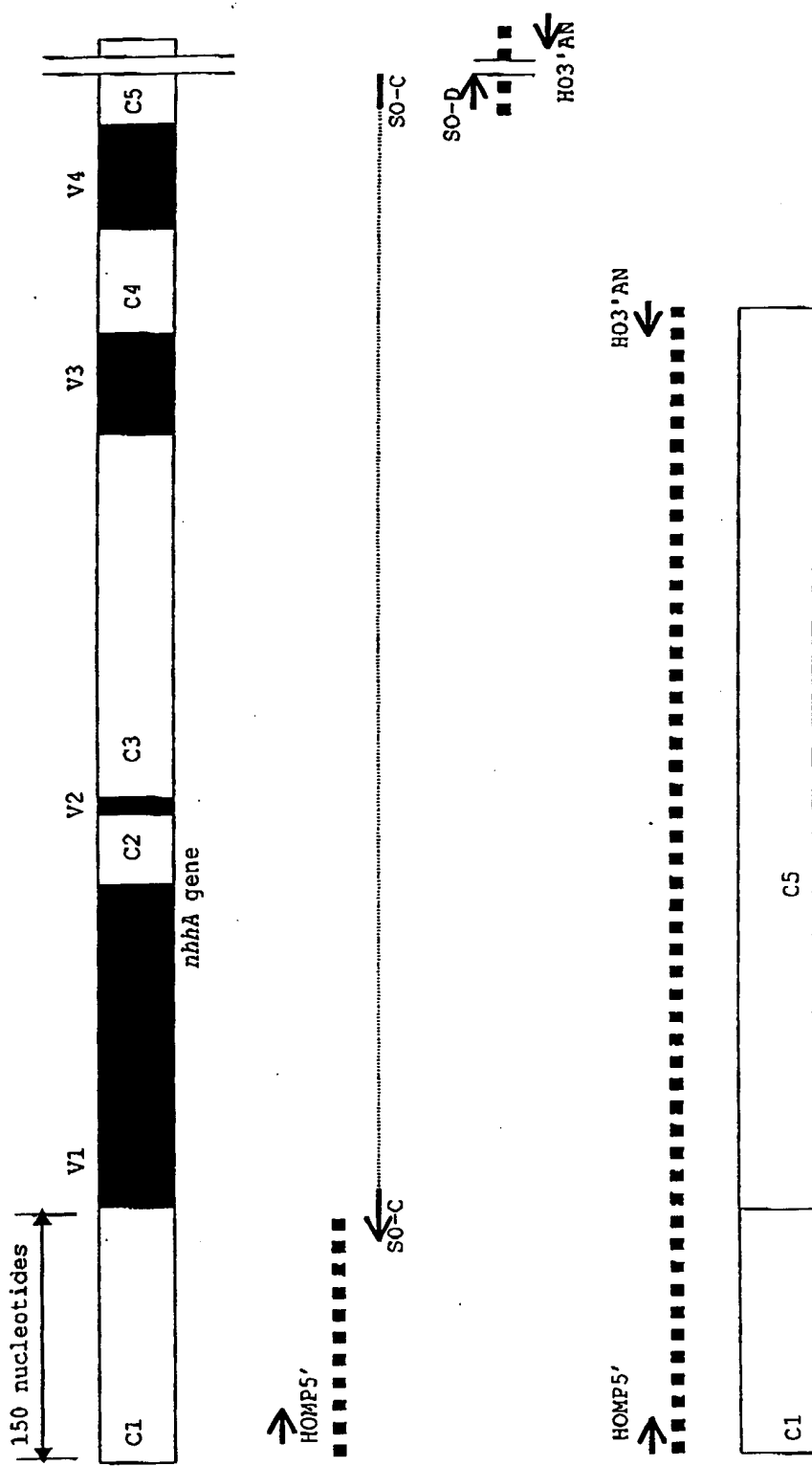


**FIG. 3A**

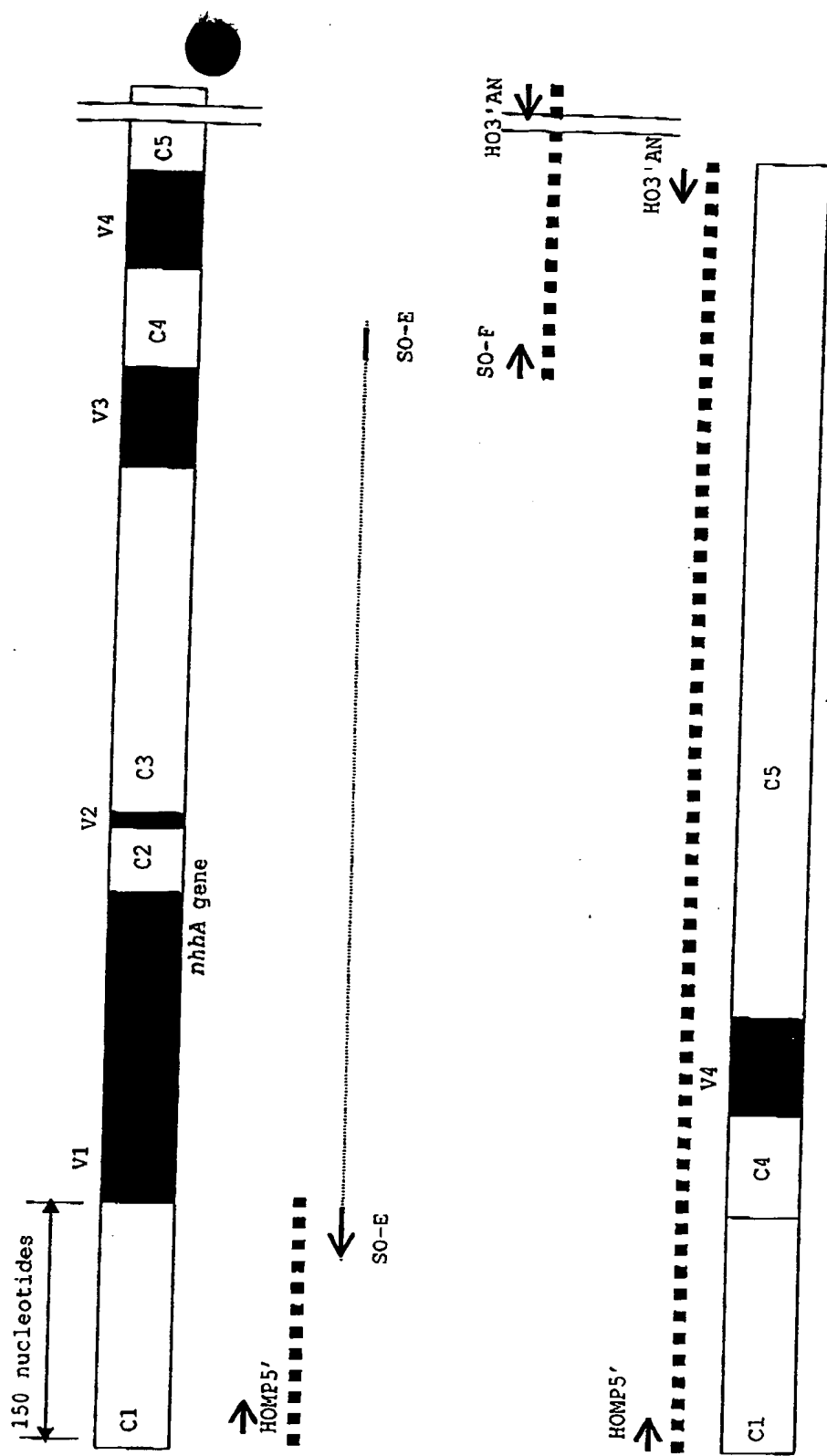
PIP52 (PMC21)



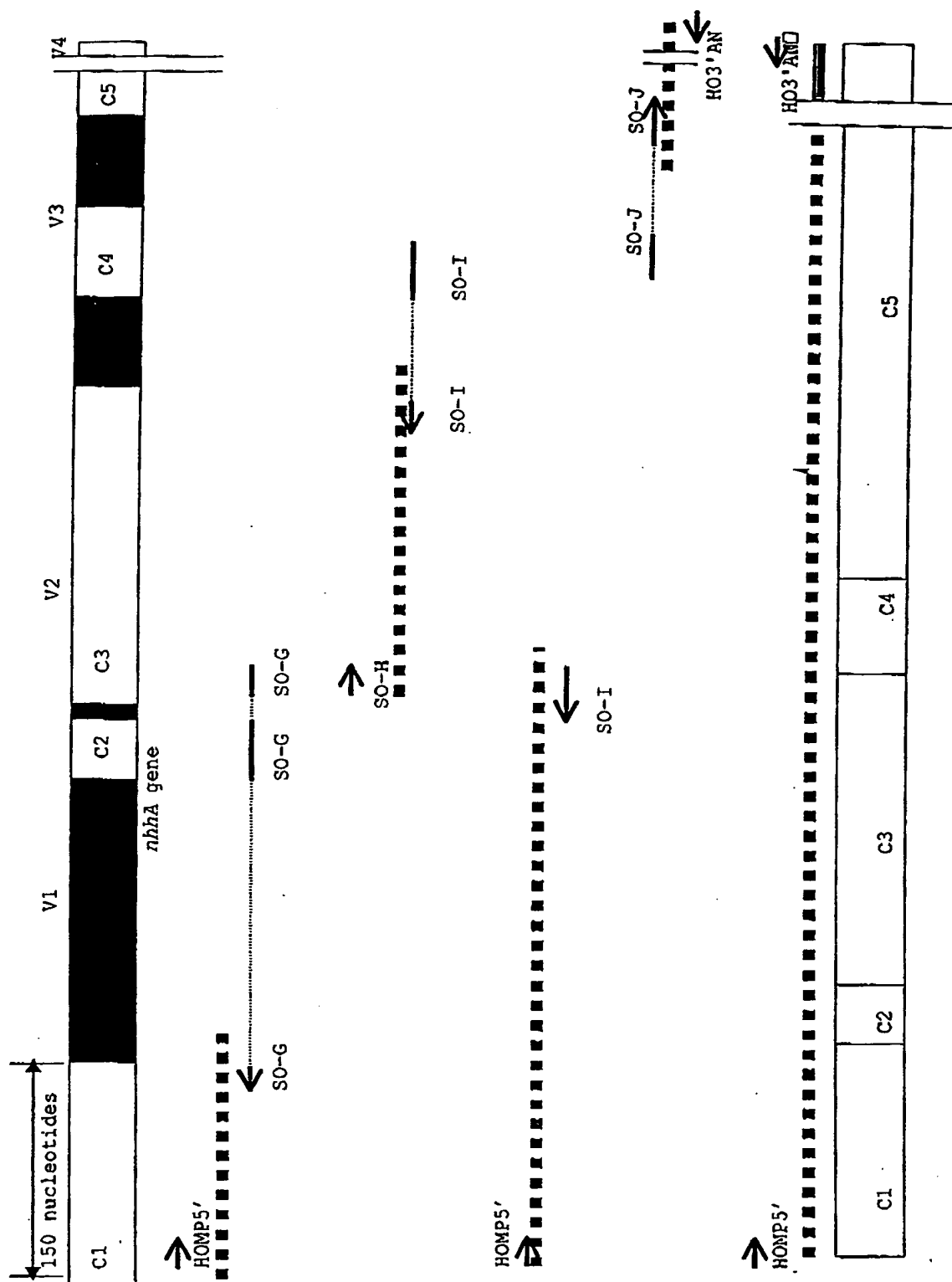
**FIG. 3B**



**FIG. 4A**



**FIG. 4B**



**FIG. 4C**

1 MNKIYRIIWN SALNAWVVVS ELTRNHTKRA SATVKTAVLA TLLFATVQAS  
 51 ANNETDLTSV GTEKLSFSAN GNKVNITS DT KGLNFAKETA GTNGDTTVHL  
 101 NGIGSTLTD T LLNTGATTNV TNDNVT DDEK KRAASVKDVL NAGWNIKG VK  
 151 PGTTASDNVD FVRTYDTVEF LSADTKTTTV NVESKDNGKK TEVKIGAKTS  
 201 VIKEKDGKLV TGKDKGENGS STDEGEGLVT AKEVIDAVNK AGWRMKTTTA  
 251 NGQTGQADKF ETVTSGTNVT FASGKGTTAT VSKDDQGNIT VMYDVNVGDA  
 301 LNVNQLQNSG WNLDSKAVAG SSGKVISGNV SPSKGKMD ET VNINAGNNIE  
 351 ITRNGKNIDI ATSMTPQFSS VSLGAGADAP TLSVDGDALN VGSKKDNKPV  
 401 RITNVAPGVK EGDVTNVAQL KGVAQNLNRR IDNVDGNARA GIAQAIATAG  
 451 LVQAYLP GKS MMAIGGGTYR GEAGYAIGYS SISDGGNWII KGTASGNSRG  
 501 HFGASASVG Y QW\*

**A**

1 ATGAACAAAA TATACCGCAT CATTTGGAAT AGTGCCCTCA ATGCATGGGT  
 51 CGTCGTATCC GAGCTCACAC GCAACCACAC CAAACGCGCC TCCGCAACCC  
 101 TGAAGACCGC CGTATTGGCG ACTCTGTTGT TTGCAACGGT TCAGGCAAGT  
 151 GCTAACAAATG AAACAGATCT GACCA GTGTT GGAAC TGAAA AATTATCGTT  
 201 TAGCGCAAAC GGCAATAAAG TCAACATCAC AAGCGACACC AAAGGCTTGA  
 251 ATTTTGCGAA AGAAACGGCT GGGACGAACG GCGACACCAC GGTTCATCTG  
 301 AACGGTATTG GTTCGACTTT GACCGATACG CTGCTGAATA CCGGAGCGAC  
 351 CACAAACGTA ACCAACGACA ACGTTACCGA TGACGAGAAA AAACGTGCGG  
 401 CAAGCGTTAA AGACGTATTA AACGCTGGCT GGAACATTAA AGGCGTTAAA  
 451 CCCGGTACAA CAGCTTCCGA TAACGTTGAT TTCGTCCGCA CTTACGACAC  
 501 AGTCGAGTTC TTGAGCGCAG ATACGAAAAC AACGACTGTT AATGTGGAAA  
 551 GCAAAGACAA CGGCAAGAAA ACCGAAGTTA AAATCGGTGC GAAGACTTCT  
 601 GTTATTAAAG AAAAAGACGG TAAGTTGGTT ACTGGTAAAG ACAAGGCGA  
 651 GAATGGTTCT TCTACAGACG AAGCGGAAGG CTTAGTGACT GCAAAGAAG  
 701 TGATTGATGC AGTAAACAAG GCTGGTTGGA GAATGAAAAC AACAAACGCT  
 751 AATGGTCAAA CAGGTCAAGC TGACAAGTTT GAAACCGTTA CATCAGGCAC  
 801 AAATGTAACC TTTGCTAGTG GTAAAGGTAC AACTGCGACT GTAAGTAAAG  
 851 ATGATCAAGG CAACATCACT GTTATGTATG ATGTAAATGT CGGCGATGCC  
 901 CTAAACGTCA ATCAGCTGCA AAACAGCGGT TGGAAATTTGG ATTCCAAAGC  
 951 GGTTCAGGT TCTTCGGGCA AAGTCATCAG CGGCAATGTT TCGCCGAGCA  
 1001 AGGGAAAGAT GGATGAAACC GTCAACATTA ATGCCGGCAA CAACATCGAG  
 1051 ATTACCCGCA ACGGTAAAAA TATCGACATC GCCACTTCGA TGACCCCGCA  
 1101 GTTTTCCAGC GTTTCGCTCG GCGCGGGGGC GGATGCGCCC ACTTTGAGCG  
 1151 TGGATGGGGA CGCATTGAAT GTCGGCAGCA AGAAGGACAA CAAACCCGTC  
 1201 CGCATTACCA ATGTCGCCCC GGGCGTTAAA GAGGGGGATG TTACAAACGT  
 1251 CGCACAACCT AAAGGCGTGG CGCAAACTT GAACAACCGC ATCGACAATG  
 1301 TGGACGGCAA CGCGCGTGCG GGCATCGCCC AAGCGATTGC AACC GCAGGT  
 1351 CTGTTTCAGG CGTATTTGCC CGGCAAGAGT ATGATGGCGA TCGGCGGCGG  
 1401 CACTTATCGC GGC GAAGCCG GTTACGCCAT CGGCTACTCC AGTATTTCCG  
 1451 ACGGCGGAAA TTGGATTATC AAAGGCACGG CTTCCGGCAA TTCGCGCGGC  
 1501 CATTTCGGTG CTTCCGCATC TGTCGGTTAT CAGTGGTAA

**B**

**FIG. 5**



1 MNKIYRIIWN SALNAWVAVS ELTRNHTKRA SATVKTAVLA TLLFATVQAN  
 51 ATDETGLINV ETEKLSFGAN GKKVNIISDT KGLNFAKETA GTNGDTTVHL  
 101 NGIGSTLTDM LLNTGATTNV TNDNVTDEK KRAASVKDVL NAGWNIKGVK  
 151 PGTASDNVD FVRTYDTVEF LSADTKTTTV NVESKDNGKK TEVKIGAKTS  
 201 VIKEDGKLV TGKGKGNGS STDEGEGLVT AKEVIDAVNK AGWRMKTSTA  
 251 NGQTGQADKF ETVTSGTKVT FASGNGTTAT VSKDDQGNIT VKYDVNVGDA  
 301 LNVNQLQNSG WNLDKAVAG SSGKVISGNV SPSKGKMDET VNINAGNNIE  
 351 ITRNGKNIDI ATSMTPQFSS VSLGAGADAP TLSVDDEGAL NVGSKDANKP  
 401 VRITNVAPGV KEGDVTNVAQ LKGVAQNLNN RIDNVNGNAR AGIAQAIATA  
 451 GLVQAYLPGK SMMAIGGGTY LGEAGYAIGY SSISAGGNWI IKGTASGNSR  
 501 GHFGASASVG YQW\*

**A**

1 ATGAACAAAA TATACCGCAT CATTTGGAAT AGTGCCCTCA ATGCCTGGGT  
 51 CGCCGTATCC GAGCTCACAC GCAACCACAC CAAACGCGCC TCCGCAACCG  
 101 TGAAGACCGC CGTATTGGCG ACACGTGTGT TTGCAACGGT TCAGGCGAAT  
 151 GCTACCGATG AAACAGGCCT GATCAATGTT GAAACTGAAA AATTATCGTT  
 201 TGGCGCAAAAC GGCAAGAAAG TCAACATCAT AAGCGACACC AAAGGCTTGA  
 251 ATTTTCGCGAA AGAAACGGCT GGGACGAACG GCGACACCAC GGTTCATCTG  
 301 AACGGTATCG GTTCGACTTT GACCGATATG CTGCTGAATA CCGGAGCGAC  
 351 CACAAACGTA ACCAACGACA ACGTTACCGA TGACGAGAAA AAACGTGCGG  
 401 CAAGCGTTAA AGACGTATTA AACGCAGGCT GGAACATTAA AGGCGTTAAA  
 451 CCCGGTACAA CAGCTTCCGA TAACGTTGAT TTCGTCCGCA CTTACGACAC  
 501 AGTCGAGTTC TTGAGCGCAG ATACGAAAAC AACGACTGTT AATGTGGAAA  
 551 GCAAAGACAA CGGCAAGAAA ACCGAAGTTA AAATCGGTGC GAAGACTTCT  
 601 GTTATTAAAG AAAAAGACGG TAAGTTGGTT ACTGGTAAAG GCAAAGGCGA  
 651 GAATGGTTCT TCTACAGACG AAGGCGAAGG CTTAGTGACT GCAAAGAGAG  
 701 TGATTGATGC AGTAAACAAG GCTGGTTGGA GAATGAAAAC AACCAACCGT  
 751 AATGGTCAAA CAGGTCAAGC TGACAAGTTT GAAACCGTTA CATCAGGCAC  
 801 AAAAGTAACC TTTGCTAGTG GTAATGGTAC AACTGCGACT GTAAGTAAAG  
 851 ATGATCAAGG CAACATCACT GTTAAGTATG ATGTAAATGT CGGCGATGCC  
 901 CTAAACGTCA ATCAGCTGCA AAACAGCGGT TGGAAATTTGG ATTCCAAAGC  
 951 GGTGCGAGGT TCTTCGGGCA AAGTCATCAG CGGCAATGTT TCGCCGAGCA  
 1001 AGGGAAAGAT GGATGAAACC GTCAACATTA ATGCCGGCAA CAACATCGAG  
 1051 ATTACCCGCA ACGGCAAAAA TATCGACATC GCCACTTCGA TGACCCCGCA  
 1101 ATTTTCCAGC GTTTCGCTCG GCGCGGGGGC GGATGCGCCC ACTTTAAGCG  
 1151 TGGATGACGA GGGCGCGTTG AATGTCGGCA GCAAGGATGC CAACAAACCC  
 1201 GTCCGCATTA CCAATGTCGC CCCGGGCGTT AAAGAGGGGG ATGTTACAAA  
 1251 CGTCGCGCAA CTTAAAGGTG TGGCGCAAAA CTTGAACAAC CGCATCGACA  
 1301 ATGTGAACGG CAACGCGCGT GCGGGCATCG CCCAAGCGAT TGCAACCGCA  
 1351 GGTCTGGTTC AGGCGTATCT GCCCGGCAAG AGTATGATGG CGATCGGCGG  
 1401 CGGCACTTAT CTCGGCGAAG CCGGTTATGC CATCGGCTAC TCAAGCATT  
 1451 CCGCCGGCGG AAATTGGATT ATCAAAGGCA CGGCTTCCGG CAATTCGCGC  
 1501 GGCCATTTTC GTGCTTCCGC ATCTGTCGGT TATCAGTGGT AA

**B**

**FIG. 6**

1 MNKIYRIIWN SALNAWVVVS ELTRNHTKRA SATVKTAFLA TLLFATVQAS  
 51 ANNVDVFTY DTVEFLSADT KTTTVNVESK DNGKKTEVKI GAKTSVIKEK  
 101 DGKLVTKGDK GENGSSTDEG EGLVTAKEVI DAVNKAGWRM KTTTANGQTG  
 151 QADKFETVTS GTNVTFASGK GTTATVSKDD QGNITVMYDV NVGDALNVNQ  
 201 LQNSGWNLDs KAVAGSSGKV ISGNVSPSKG KMDETVNINA GNNIEITRNG  
 251 KNIDIATSMT PQFSSVSLGA GADAPTLSVD GDALNVGSKK DNKPVRIITNV  
 301 APGVKEGDVT NVAQLKGVAQ NLNNRIDNVD GNARAGIAQA IATAGLVQAY  
 351 LPGKSMAIG GGTyrGEAGY AIGYSSISDG GNWIKGTAS GNSRGHFGAS  
 401 ASVGyQW\*

**A**

1 ATGAACAAAA TATACCGCAT CATTGGAAT AGTGCCCTCA ATGCATGGGT  
 51 CGTCGTATCC GAGCTCACAC GCAACCACAC CAAACGCGCC TCCGCAACCG  
 101 TGAAGACCGC CGTATTGGCG ACTCTGTTGT TTGCAACGGT TCAGGCAAGT  
 151 GCTAACACG TGTATTTCGT CCGCACTTAC GACACAGTCG AGTTCTTGAG  
 201 CGCAGATACG AAAACAACGA CTGTAAATGT GGAAAGCAAA GACAACGGCA  
 251 AGAAAACCGA AGTTAAAATC GGTGCGAAGA CTCTGTAT TAAAGAAAAA  
 301 GACGGTAAGT TGGTACTGG TAAAGACAAA GGCGAGAATG GTTCTTCTAC  
 351 AGACGAAGGC GAAGGCTTAG TGAATGAAA AGAAGTGATT GATGCAGTAA  
 401 ACAAGGCTGG TTGGAGAATG AAAACAACAA CCGCTAATGG TCAACAGGT  
 451 CAAGCTGACA AGTTTGAAAC CGTTACATCA GGCACAAATG TAACCTTTGC  
 501 TAGTGGTAAA GGTACAACG CGACTGTAAG TAAAGATGAT CAAGGCAACA  
 551 TCACTGTTAT GTATGATGTA AATGTCGGCG ATGCCCTAAA CGTCAATCAG  
 601 CTGCAAAACA GCGGTTGGAA TTTGGATTCC AAAGCGGTTG CAGGTTCTTC  
 651 GGGCAAAGTC ATCAGCGGCA ATGTTTCGCC GAGCAAGGGA AAGATGGATG  
 701 AAACCGTCAA CATTAAATGCC GGCAACAACA TCGAGATTAC CCGCAACGGT  
 751 AAAAATATCG ACATCGCCAC TTCGATGACC CCGCAGTTTT CCAGCGTTTC  
 801 GCTCGGCGCG GGGGCGGATG CGCCCACTTT GAGCGTGGAT GGGGACGCAT  
 851 TGAATGTCGG CAGCAAGAAG GACAACAAC CCGTCCGCAT TACCAATGTC  
 901 GCCCCGGGCG TTAAAGAGGG GGATGTTACA AACGTCGCAC AACTTAAAGG  
 951 CGTGGCGCAA AACTTGAACA ACCGCATCGA CAATGTGGAC GGCAACGCGC  
 1001 GTGCGGGCAT CGCCCAAGCG ATTGCAACCG CAGGTCTGGT TCAGGCGTAT  
 1051 TTGCCCCGCA AGAGTATGAT GGCATCGGC GCGGCGACTT ATCGCGGCGA  
 1101 AGCCGGTTAC GCCATCGGCT ACTCCAGTAT TTCCGACGGC GGAAATTGGA  
 1151 TTATCAAAGG CACGGCTTCC GGCAATTCGC GCGGCCATTT CGGTGCTTCC  
 1201 GCATCTGTCT GTTATCAGTG GTAA

**B**

**FIG. 7**

1 MNKIYRIIW SALNAWVVVS ELTRNHTKRA SATVKTAVLA TLLFATVQAS  
 51 ANRAASVKDV LNAGWNIKGV KPGTTASDNV DFVRTYDTVE FLSADTKTTT  
 101 VNVESKDNGK KTEVKIGAKT SVIKEKDGL VTGKDKGENG SSTDEGEGLV  
 151 TAKEVIDAVN KAGWRMKTTT ANGQTGQADK FETVTSGTNV TFASGKGTTA  
 201 TVSKDDQGNL TVMYDVNVGD ALNVNQLQNS GWNLDKAVA GSSGKVISGN  
 251 VSFSKGKMDL TVNINAGNNI EITRNGKNID IATSMTPQFS SVSLGAGADA  
 301 PTLSDVDGAL NVGSKKDNKP VRITNVAPGV KEGDVTNVAQ LKGVAQNLNN  
 351 RIDNVDGNAR AGIAQAIATA GLVQAYLPK SMMAIGGGTY RGEAGYAIGY  
 401 SSISDGGNWI IKG TASGNSR GHFGASASVG YQW\*

**A**

1 ATGAACAAAA TATACCGCAT CATTGGAAT AGTGCCCTCA ATGCATGGGT  
 51 CGTCGTATCC GAGCTCACAC GCAACACAC CAAACGCGCC TCCGCAACCG  
 101 TGAAGACCGC CGTATTGGCG ACTCTGTTGT TTGCAACGGT TCAGGCAAGT  
 151 GCTAACCGTG CGGCAAGCGT TAAAGACGTA TTAAACGCTG GCTGGAACAT  
 201 TAAAGGCGTT AAACCCGGTA CAACAGCTTC CGATAACGTT GATTTCGTCC  
 251 GCACTTACGA CACAGTCGAG TTCTTGAGCG CAGATACGAA AACCAAGACT  
 301 GTTAATGTGG AAAGCAAAGA CAACGGCAAG AAAACCGAAG TTAAATCGG  
 351 TGCGAAGACT TCTGTTATTA AAGAAAAAGA CCGTAAGTTG GTTACTGGTA  
 401 AAGACAAAGG CGAGAATGGT TCTTCTACAG ACGAAGGCGA AGGCTTAGTG  
 451 ACTGCAAAAAG AAGTGATTGA TGCAGTAAAC AAGGCTGGTT GGAGAATGAA  
 501 AACAAACAACC GCTAATGGTC AAACAGGTCA AGCTGACAAG TTTGAAACCG  
 551 TTACATCAGG CACAAATGTA ACCTTTGCTA GTGGTAAAGG TACAACGCG  
 601 ACTGTAAGTA AAGATGATCA AGGCAACATC ACTGTTATGT ATGATGTAAA  
 651 TGTGCGCGAT GCCCTAAACG TCAATCAGCT GCAAAACAGC GGTGGAATT  
 701 TGGATTCCAA AGCGGTTGCA GGTCTTCGG GCAAAGTCAT CAGCGGCAAT  
 751 GTTTCGCCGA GCAAGGGAAA GATGGATGAA ACCGTCAACA TTAATGCCGG  
 801 CAACAACATC GAGATTACCC GCAACGGTAA AAATATCGAC ATCGCCACTT  
 851 CGATGACCCC GCAGTTTCC AGCGTTTCGC TCGGCGCGGG GCGGATGCG  
 901 CCCACTTTGA GCGTGGATGG GGACGCATTG AATGTCGGCA GCAAGAAGGA  
 951 CAACAAACCC GTCCGCATTA CCAATGTCGC CCCGGGCGTT AAAGAGGGGG  
 1001 ATGTTACAAA CGTCGCACAA CTTAAAGGCG TGGCGCAAAA CTTGAACAAC  
 1051 CGCATCGACA ATGTGGACGG CAACGCGCGT GCGGGCATCG CCAAGCGAT  
 1101 TGCAACCGCA GGTCTGGTTC AGGCGTATTT GCGCGGCAAG AGTATGATGG  
 1151 CGATCGGCGG CCGCACTTAT CGCGGCGAAG CCGGTTACGC CATCGGCTAC  
 1201 TCCAGTATTT CCGACGGCGG AAATTEGATT ATCAAAGGCA CGGCTTCCGG  
 1251 CAATTCGCGC GGCCATTTCG GTGCTTCCGC ATCTGTCGGT TATCAGTGGT  
 1301 AA

**B**

**FIG. 8**

1 MNKIYRIIWN SALNAWVVVS ELTRNHTKRA SATVKTAVLA TLLFATVQAS  
 51 ANTLKAGDNL KIKQFTYSLK KDLTDLTSVG TEKLSFSANG NKVNITSDTK  
 101 GLNFAKETAG TNGDTPVHLN GIGSTLTDRA ASVKDVLNAG WNIKGVKNVD  
 151 FVRTYDTVEF LSADTKTTTV NVEKDNKGKK TEVKIGAKTS VIKEDGKLV  
 201 TGKDKGENGS STDEGEGLVT AKEVIDAVNK AGWRMKTTTA NGQTGQADKF  
 251 ETVTSGTNVT FASGKGTTAT VSKDDQGNIT VMYDVNVGDA LNVNQLQNSG  
 301 WNLDSKAVAG SSGKVISGNV SPSKGKMDET VNINAGNNIE ITRNGKNIDI  
 351 ATSMTPQFSS VSLGAGADAP TLSVDGDALN VGSKKDNKPV RITNVAPGVK  
 401 EGDVTNVAQL KGVAQNLNLR IDNVDGNARA GIAQAIATAG LVQAYLPGKS  
 451 MMAIGGGTYR GEAGYAIGYS SISDGGNWII KGTASGNSRG HFGASASVGY  
 501 QW\*

**A**

1 ATGAACAAAA TATACCGCAT CATTTGGAAT AGTGCCCTCA ATGCATGGGT  
 51 CGTCGTATCC GAGCTCACAC GCAACCACAC CAAACGCGCC TCCGCAACCG  
 101 TGAAGACCGC CGTATTGGCG ACTCTGTTGT TTGCAACGGT TCAGGCAAGT  
 151 GCTAACACCC TCAAAGCCGG CGACAACCTG AAAATCAAAC AATTCACCTA  
 201 CTCGCTGAAA AAAGACCTCA CAGATCTGAC CAGTGTGGA ACTGAAAAAT  
 251 TATCGTTTAG CGCAAACGGC AATAAAGTCA ACATCACAAG CGACACCAAA  
 301 GGCTTGAATT TTGCGAAAGA AACGGCTGGG ACGAACGGCG ACACCACGGT  
 351 TCATCTGAAC GGTATTGGTT CGACTTGGAC CGATCGTGCG GCAAGCGTTA  
 401 AAGACGTATT AAACGCTGGC TGGAAACATTA AAGGCGTTAA AAACGTTGAT  
 451 TTCGTCCGCA CTTACGACAC AGTCGAGTTC TTGAGCGCAG ATACGAAAAC  
 501 AACGACTGTT AATGTGGAAA GCAAAGACAA CGGCAAGAAA ACCGAAGTTA  
 551 AAATCGGTGC GAAGACTTCT GTTATTAAAG AAAAAGACGG TAAGTTGGTT  
 601 ACTGGTAAAG ACAAGGCGA GAATGGTTCT TCTACAGACG AAGGCGAAGG  
 651 CTTAGTGAAT GCAAAAGAAG TGATTGATGC AGTAAACAAG GCTGGTTGGA  
 701 GAATGAAAAC AACAACCGCT AATGGTCAAA CAGGTCAAGC TGACAAGTTT  
 751 GAAACCGTTA CATCAGGCAC AAATGTAACC TTTGCTAGTG GTAAAGGTAC  
 801 AACTGCGACT GTAAGTAAAG ATGATCAAGG CAACATCACT GTTATGTATG  
 851 ATGTAAATGT CGGCGATGCC CTAAACGTCA ATCAGCTGCA AAACAGCGGT  
 901 TGGAAATTTG ATTCCAAAGC GGTTCGAGGT TCTTCGGGCA AAGTCATCAG  
 951 CGGCAATGTT TCGCCGAGCA AGGGAAAGAT GGATGAAACC GTCAACATTA  
 1001 ATGCCCGCAA CAACATCGAG ATTACCCGCA ACGGTAAAAA TATCGACATC  
 1051 GCCACTTCGA TGACCCCGCA GTTTTCCAGC GTTTCGCTCG GCGCGGGGGC  
 1101 GGATGCGCCC ACTTTGAGCG TGGATGGGGA CGCATTGAAT GTCGGCAGCA  
 1151 AGAAGGACAA CAAACCCGTC CGCATTACCA ATGTCGCCCC GGGCGTTAAA  
 1201 GAGGGGGATG TTACAAACGT CGCACAACTT AAAGGCGTGG CGCAAACTT  
 1251 GAACAACCGC ATCGACAATG TGGACGGCAA CGCGCGTGCG GGCATCGCCC  
 1301 AAGCGATTGC AACCAGAGGT CTGGTTCAGG CGTATTTGCC CGGCAAGAGT  
 1351 ATGATGGCGA TCGGCGGCGG CACTTATCGC GCGGAAGCCG GTTACGCCAT  
 1401 CGGCTACTCC AGTATTTCCG ACGGCGGAAA TTGGATTATC AAAGGCACGG  
 1451 CTTCCGGCAA TTCGCGCGGC CATTTCCGGT CTTCGCGATC TGTCGGTTAT  
 1501 CAGTGGTAA

**B**

**FIG. 9**

1 50  
H41 MNKIYRIWN SALNAWVAVS ELTRNHTKRA SATVKTAVLA TLLFATVOAN  
PMC21 MNKIYRIWN SALNAWVAVS ELTRNHTKRA SATVKTAVLA TLLFATVOAN  
H41Studel MNKIYRIWN SALNAWVAVS ELTRNHTKRA SATVKTAVLA TLLFATVOAN  
PMC21Bgldel MNKIYRIWN SALNAWVAVS ELTRNHTKRA SATVKTAVLA TLLFATVOAN  
PMC21C1C5 MNKIYRIWN SALNAWVAVS ELTRNHTKRA SATVKTAVLA TLLFATVOAN  
C1

51 100  
H41 ATDED...EEE ELESVQRS.V VGSIOASMEG SVELET...I SLSMTNDSKE  
PMC21 ANNEEQEYEL YLHPVORTVA VLIVNSDKEG AGEKEKVEEN SDWAVYFNEK  
H41Studel ATDE.....  
PMC21Bgldel ANNE.....  
PMC21C1C5 AN.....  
V1

101 150  
H41 FVDPYIVVTI KAGDNLKIKO N.TNENTNAS SFTYSLKKDL TGLINVETEK  
PMC21 GVLTAIREITL KAGDNLKIKO NGTN.....FTYSLKKDL TDLTSVGTEK  
H41Studel ..... TGLINVETEK  
PMC21Bgldel ..... TDLTSVGTEK  
PMC21C1C5 .....  
V1 C2 V2 C3

151 200  
H41 LSFGANGKKV NIISDTKGLN FAKETAGTNG DTTVHLNGIG STLTDMLLNT  
PMC21 LSFSAHGKVV NITS DT KGLN FAKETAGTNG DTTVHLNGIG STLTDTLLNT  
H41Studel LSFGANGKKV NIISDTKGLN FAKETAGTNG DTTVHLNGIG STLTDMLLNT  
PMC21Bgldel LSFSANGKVV NITS DT KGLN FAKETAGTNG DTTVHLNGIG STLTDTLLNT  
PMC21C1C5 .....  
C3 V3

201 250  
H41 GATTNVTNDN VTDDEKKRAA SVKDVLNAGW NIKGVKPGTT ASDNVDFVRT  
PMC21 GATTNVTNDN VTDDEKKRAA SVKDVLNAGW NIKGVKPGTT ASDNVDFVRT  
H41Studel GATTNVTNDN VTDDEKKRAA SVKDVLNAGW NIKGVKPGTT ASDNVDFVRT  
PMC21Bgldel GATTNVTNDN VTDDEKKRAA SVKDVLNAGW NIKGVKPGTT ASDNVDFVRT  
PMC21C1C5 .....NVDFVRT  
V3 C4 V4 C5

251 300  
H41 YDTVEFLSAD TKTTTVNVES KDNGKKTEVK IGAKTSVIKE KDGKLVGTGK  
PMC21 YDTVEFLSAD TKTTTVNVES KDNGKKTEVK IGAKTSVIKE KDGKLVGTGK  
H41Studel YDTVEFLSAD TKTTTVNVES KDNGKKTEVK IGAKTSVIKE KDGKLVGTGK  
PMC21Bgldel YDTVEFLSAD TKTTTVNVES KDNGKKTEVK IGAKTSVIKE KDGKLVGTGK  
PMC21C1C5 YDTVEFLSAD TKTTTVNVES KDNGKKTEVK IGAKTSVIKE KDGKLVGTGK  
C5

301 350  
H41 KGENGSSIDE GEGLVTAKEV IDAVNKAGWR MKTTTANGQT GOADKFETVT  
PMC21 KGENGSSIDE GEGLVTAKEV IDAVNKAGWR MKTTTANGQT GOADKFETVT  
H41Studel KGENGSSIDE GEGLVTAKEV IDAVNKAGWR MKTTTANGQT GOADKFETVT  
PMC21Bgldel KGENGSSIDE GEGLVTAKEV IDAVNKAGWR MKTTTANGQT GOADKFETVT  
PMC21C1C5 KGENGSSIDE GEGLVTAKEV IDAVNKAGWR MKTTTANGQT GOADKFETVT  
C5

351 400  
H41 SGTKVTFASG NGTTATVSKD DQGNITVKYD VNVGDALNVN QLQNSGWNLD  
PMC21 SGTNVTFASG KGTATVSKD DQGNITVMYD VNVGDALNVN QLQNSGWNLD  
H41Studel SGTKVTFASG NGTTATVSKD DQGNITVKYD VNVGDALNVN QLQNSGWNLD  
PMC21Bgldel SGTNVTFASG KGTATVSKD DQGNITVMYD VNVGDALNVN QLQNSGWNLD  
PMC21C1C5 SGTNVTFASG KGTATVSKD DQGNITVMYD VNVGDALNVN QLQNSGWNLD  
C5

FIG. 10

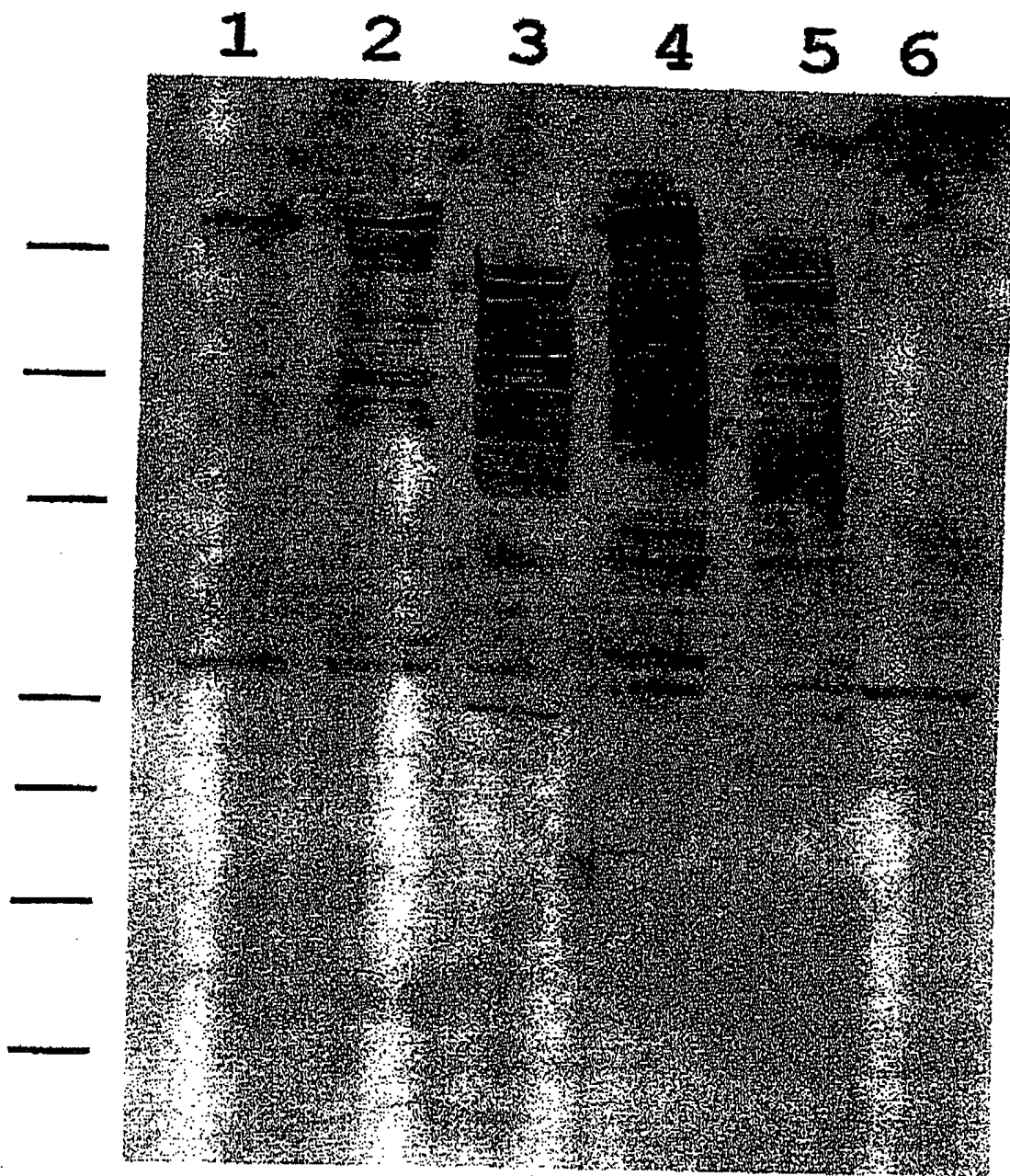
401 450  
H41 SKAVAGSSGK VISGNVSPSK GKMDETVNIN AGNNIEITRN GKNIDIATSM  
PMC21 SKAVAGSSGK VISGNVSPSK GKMDETVNIN AGNNIEITRN GKNIDIATSM  
H41Studel SKAVAGSSGK VISGNVSPSK GKMDETVNIN AGNNIEITRN GKNIDIATSM  
PMC21Bgldel SKAVAGSSGK VISGNVSPSK GKMDETVNIN AGNNIEITRN GKNIDIATSM  
PMC21C1C5 SKAVAGSSGK VISGNVSPSK GKMDETVNIN AGNNIEITRN GKNIDIATSM  
C5

451 500  
H41 TPQFSSVSLG AGADAPTLV DDEGALNVGS KDANKPVRT NVAPGVKEGD  
PMC21 TPQFSSVSLG AGADAPTLV DG.DALNVGS KKDNKPVRT NVAPGVKEGD  
H41Studel TPQFSSVSLG AGADAPTLV DDEGALNVGS KDANKPVRT NVAPGVKEGD  
PMC21Bgldel TPQFSSVSLG AGADAPTLV DG.DALNVGS KKDNKPVRT NVAPGVKEGD  
PMC21C1C5 TPQFSSVSLG AGADAPTLV DG.DALNVGS KKDNKPVRT NVAPGVKEGD  
C5

501 550  
H41 VTNVAQLKGV AQNLNNRIDN VNGNARAGIA QAIATAGLVQ AYLPGKSMMMA  
PMC21 VTNVAQLKGV AQNLNNRIDN VDGNNARAGIA QAIATAGLVQ AYLPGKSMMMA  
H41Studel VTNVAQLKGV AQNLNNRIDN VNGNARAGIA QAIATAGLVQ AYLPGKSMMMA  
PMC21Bgldel VTNVAQLKGV AQNLNNRIDN VDGNNARAGIA QAIATAGLVQ AYLPGKSMMMA  
PMC21C1C5 VTNVAQLKGV AQNLNNRIDN VDGNNARAGIA QAIATAGLVQ AYLPGKSMMMA  
C5

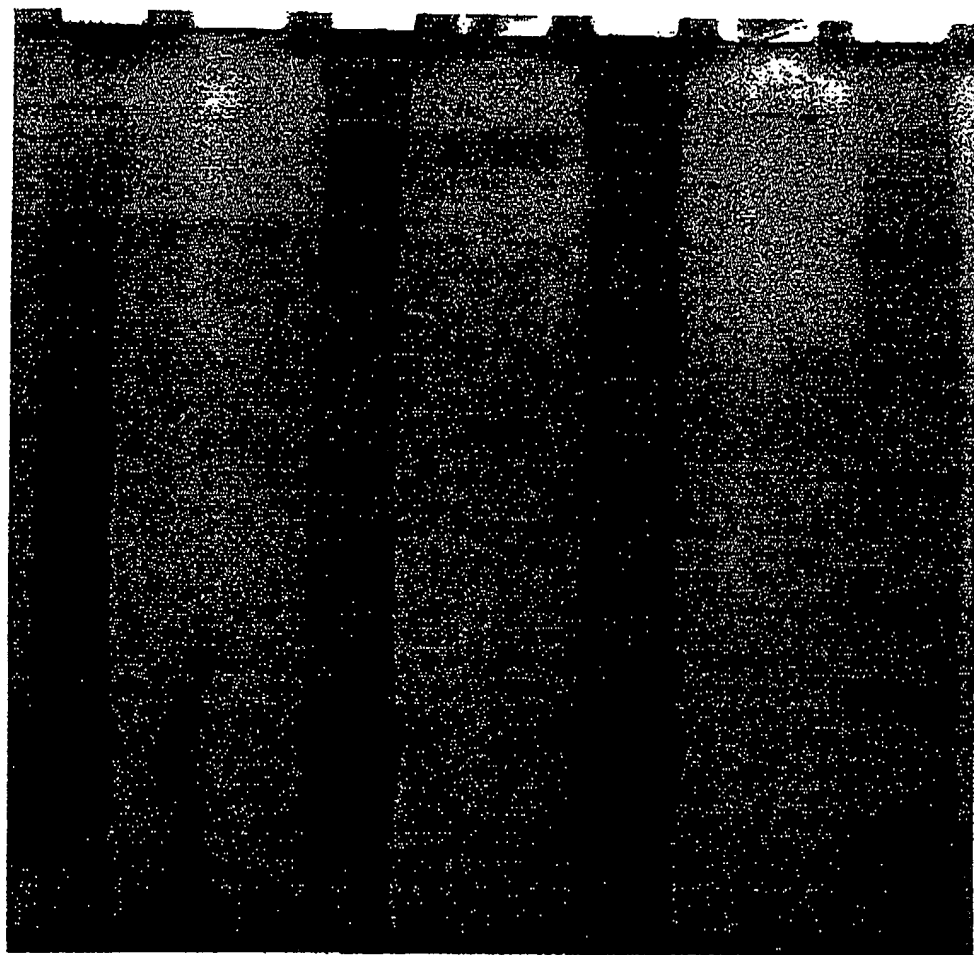
551 600  
H41 IGGGTYLGEA GYAIGYSSIS AGGNWIIKGT ASGNSRGHFG ASASVGYQW.  
PMC21 IGGGTYRGEA GYAIGYSSIS DGGNWIIGKT ASGNSRGHFG ASASVGYQW.  
H41Studel IGGGTYLGEA GYAIGYSSIS AGGNWIIKGT ASGNSRGHFG ASASVGYQW.  
PMC21Bgldel IGGGTYRGEA GYAIGYSSIS DGGNWIIGKT ASGNSRGHFG ASASVGYQW.  
PMC21C1C5 IGGGTYRGEA GYAIGYSSIS DGGNWIIGKT ASGNSRGHFG ASASVGYQW.  
C5

**FIG. 10 cont'd**



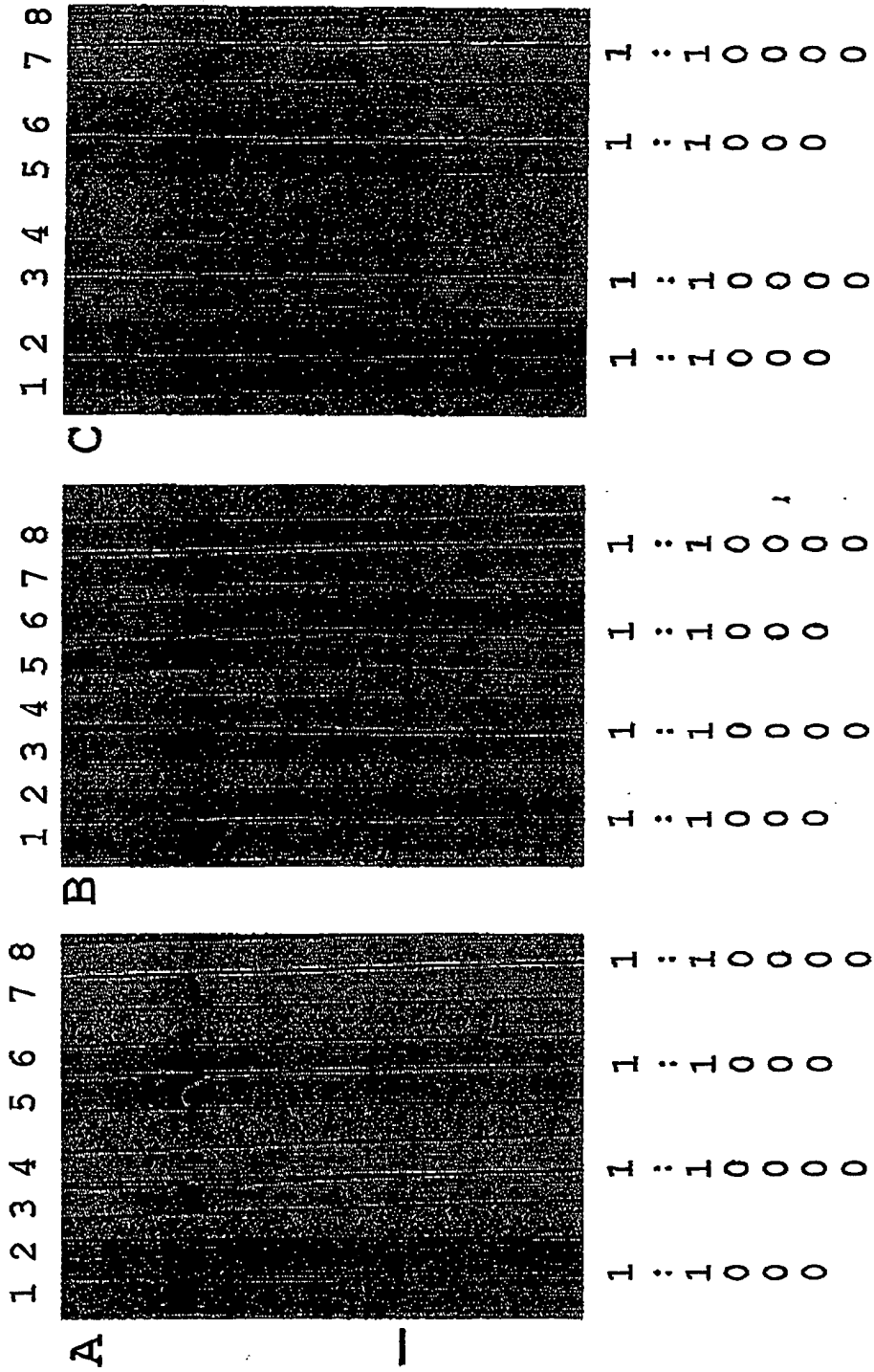
**FIG. 11**

1 2 3 4 5 6 7



**FIG. 12**





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FIG. 13

**A**

52 NNEEQEEYL YLHPVQRTVA VLIVNSDKEG AGEKEKVEEN SDWAVYFNEK  
101 GVLTAIREITL KAGDNLKIKQ NGTNFTYSLK KDLTDLTSVG TEKLSFSAHG  
151 NKVNITSDTK GLNFAKETAG TNGDTTVHLN GIGSTLTDTL LNTGATTNVT  
201 NDNVTDDEKK RAASVKDVLN AGWNIKGVPK GTTASDNVDF VRTYDTVEFL  
251 SADTKTTTVN VESKDNGKKT EVKIGAKTSV IKEKDGLVLT GKDKGENGSS  
301 TDEGEGLVTA KEVIDAVNKA GWRMKTTTAN GQTGQADKFE TVTSGTNVTF  
351 ASGKGTTATV SKDDQGNITV MYDVNVGDAL NVNQLQNSGW NLDSKAVAGS  
401 SGKVISGNVS PSKKGMDETV NINAGNNIEI TRNGKNIDIA TSMT PQFSSV  
451 SLGAGADAPT LSVGDALNV GSKKDNKPVR ITNVAPGVKE GDVTNVAQLK  
501 GVAQNLLNRI DNVGDNARAG IAQAIATAGL VQAYLPGKSM MAIGGGTYRG  
551 EAGYAIGYSS ISDGGNWIIG GTASGNSRGH FGASASVGYQ W\*

**B**

52 TDEDEEEEL ESQRSVVG S IQASMEGSVE LETISLSMTN DSKEFVDPYI  
101 VVTLKAGDNL KIKQNTNENT NASSFTYSLK KDLTGLINVE TEKLSFGANG  
151 KKVNIISDTK GLNFAKETAG TNGDTTVHLN GIGSTLTDML LNTGATTNVT  
201 NDNVTDDEKK RAASVKDVLN AGWNIKGVPK GTTASDNVDF VRTYDTVEFL  
251 SADTKTTTVN VESKDNGKKT EVKIGAKTSV IKEKDGLVLT GKDKGENGSS  
301 TDEGEGLVTA KEVIDAVNKA GWRMKTTTAN GQTGQADKFE TVTSGTKVTF  
351 ASGNGTTATV SKDDQGNITV KYDVNVGDAL NVNQLQNSGW NLDSKAVAGS  
401 SGKVISGNVS PSKKGMDETV NINAGNNIEI TRNGKNIDIA TSMT PQFSSV  
451 SLGAGADAPT LSVDDGALN VGSKDANKPV RITNVAPGVK EGDVTNVAQL  
501 KGVAQNLLNR IDNVNGNARA GIAQAIATAG LVQAYLPGKS MMAIGGGTYL  
551 GEAGYAIGYS SISAGGNWII KGTASGNSRG HFGASASVGY QW\*

**FIG. 14**

C

52 NNETDLTSV GTEKLSFSAN GNKVNITS DT KGLNFAKETA GTNGDTTVHL  
101 NGIGSTLTDT LLNTGATTNV TNDNVT DDEK KRAASVKDVL NAGWNIKG VK  
151 PGTTASDNVD FVRTYDTVEF LSADTKTTTV NVESKDNGKK TEVKIGAKTS  
201 VIKKDGKLV TGKDKGENGS STDEGEGLVT AKEVIDAVNK AGWRMKTTTA  
251 NGQTGQADKF ETVTSGTNVT FASGKGTTAT VSKDDQGNIT VMYDVNVGDA  
301 LNVNQLQNSG WNLDKAVAG SSGKVISGNV SPSKGKMD ET VNINAGNNIE  
351 ITRNGKNIDI ATSMTPQFSS VSLGAGADAP TLSVDGDALN VGSKKDNKPV  
401 RITNVAPGVK EGDVTNVAQL KGVAQNLNNR IDNV DGNARA GIAQAIATAG  
451 LVQAYLPGKS MMAIGGGTYR GEAGYAIGYS SISDGGNWII KGTASGNSRG  
501 HFGASASVGY QW\*

D

52 TDETGLINV ETEKLSFGAN GKKVNIISDT KGLNFAKETA GTNGDTTVHL  
101 NGIGSTLTDM LLNTGATTNV TNDNVT DDEK KRAASVKDVL NAGWNIKG VK  
151 PGTTASDNVD FVRTYDTVEF LSADTKTTTV NVESKDNGKK TEVKIGAKTS  
201 VIKKDGKLV TGKDKGENGS STDEGEGLVT AKEVIDAVNK AGWRMKTTTA  
251 NGQTGQADKF ETVTSGTKVT FASGNGTTAT VSKDDQGNIT VKYDVNVGDA  
301 LNVNQLQNSG WNLDKAVAG SSGKVISGNV SPSKGKMD ET VNINAGNNIE  
351 ITRNGKNIDI ATSMTPQFSS VSLGAGADAP TLSVDDEGAL NVGSKDANKP  
401 VRITNVAPGV KEGDVTNVAQ LKGVAQNLNN RIDNVNGNAR AGIAQAIATA  
451 GLVQAYLPGK SMMAIGGGTY LGEAGYAIGY SSISAGGNWI IKGTASGNSR  
501 GHFGASASVG YQW\*

FIG. 14

**E**

52 NNVDFVRTY DTVEFLSADT KTTTVNVESK DNGKKTEVKI GAKTSVIEKEK  
 101 DGKLVTGKDK GENGSSTDEG EGLVTAKEVI DAVNKAGWRM KTTTANGQTG  
 151 QADKFETVTS GTNVTFASGK GTTATVSKDD QGNITVMYDV NVGDALNVNQ  
 201 LQNSGWNLDS KAVAGSSGKV ISGNVSPSKG KMDETVNINA GNNIEITRNG  
 251 KNIDIATSMT PQFSSVSLGA GADAPTLSVD GDALNVGSKK DNKPVRITNV  
 301 APGVKEGDTV NVAQLKGVAQ NLNNRIDNVD GNARAGIAQA IATAGLVQAY  
 351 LPGKSMMMAIG GGTyrGEAGY AIGYSSISDG GNWIIGKTAS GNSRGHFGAS  
 401 ASVGYQW\*

**F**

52 NRAASVKDV LNAGWNIKGV KPGTTASDNV DFVRTYDTVE FLSADTKTTT  
 101 VNVESKDNGK KTEVKIGAKT SVIEKDGKL VTGKDKGENG SSTDEGEGLV  
 151 TAKEVIDAVN KAGWRMKTTH ANGQTQADK FETVTSGTNV TFASGKGTTA  
 201 TVSKDDQGNI TVMYDVNVGD ALNVNQLQNS GWNLDSKAVA GSSGKVISGN  
 251 VSPSKGKMDE TVNINAGNNI EITRNGKNID IATSMTPQFS SVSLGAGADA  
 301 PTLSDGDAL NVGSKKDNKP VRITNVAPGV KEGDVTNVAQ LKGVAQNLLN  
 351 RIDNVDGNAR AGIAQAIATA GLVQAYLPGK SMAIGGGTY RGEAGYAIGY  
 401 SSISDGGNWI IKGTASGNSR GHFGASASVG YQW\*

**G**

50 SANTLKAGDNL KIKQFTYSLK KDLTDLTSVG TEKLSFSANG NKVNITSDTK  
 101 GLNFAKETAG TNGDTTVHLN GIGSTLTDRA ASVKDVLNAG WNIKGVKNVD  
 151 FVRTYDTVEF LSADTKTTTV NVESKDNGKK TEVKIGAKTS VIEKDGKLV  
 201 TGKDKGENGS STDEGEGLVT AKEVIDAVNK AGWRMKTTHA NGQTQADKF  
 251 ETVTSGTNVT FASGKGTTAT VSKDDQGNIT VMYDVNVGDA LNVNQLQNSG  
 301 WNLDKAVAG SSGKVISGNV SPSKGKMDET VNINAGNNIE ITRNGKNIDI  
 351 ATSMTPQFSS VSLGAGADAP TLSVDGDALN VGSKKDNKPV RITNVAPGVK  
 401 EGDVTNVAQL KGVAQNLLNR IDNVDGNARA GIAQAIATAG LVQAYLPGKS  
 451 MMAIGGGTYR GEAGYAIGYS SISDGGNWII KGTASGNSRG HFGASASVG  
 501 QW\*

**FIG. 14**